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(54) Title: NUCLEIC ACIDS, PROTEINS, AND ANTIBODIES

(57) Abstract: The present invention relates to novel musculoskeletal system related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "musculoskeletal system antigens", and the use of such musculoskeletal system antigens for detecting disorders of the musculoskeletal system, particularly the presence of cancer and cancer metastases. More specifically, isolated musculoskeletal system associated nucleic acid molecules are provided encoding novel musculoskeletal system associated polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system associated polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer of musculoskeletal tissues, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and function of the polypeptides of the present invention.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Nucleic Acids, Proteins, and Antibodies

[001] This application refers to a "Sequence Listing" that is provided only on electronic media in computer readable form pursuant to Administrative Instructions Section 801(a)(i). The Sequence Listing forms a part of this description pursuant to Rule 5.2 and Administrative Instructions Sections 801 to 806, and is hereby incorporated in its entirety.

[002] The Sequence Listing is provided as an electronic file (PC005PCT_seqList.txt, 7,563,935 bytes in size, created on January 12, 2001) on four identical compact discs (CD-R), labeled "COPY 1," "COPY 2," "COPY 3," and "CRF." The Sequence Listing complies with Annex C of the Administrative Instructions, and may be viewed, for example, on an IBM-PC machine running the MS-Windows operating system by using the V viewer software, version 2000 (see World Wide Web URL: <http://www.fileviewer.com>).

Field of the Invention

[003] The present invention relates to novel musculoskeletal system related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively referred to as "musculoskeletal system antigens," and antibodies that immunospecifically bind these polypeptides, and the use of such musculoskeletal system polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the musculoskeletal system, including, but not limited

musculoskeletal system polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system polynucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including musculoskeletal system cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

Background of the Invention

[004] The Human Musculoskeletal System is comprised of skeleton (e.g., bone), muscle, tendon, ligament, and other components of joints, which constitute the basic structural framework of the body. Together, the components of this system provide the strength, stability, frame, and elasticity necessary for movement. Additionally, the musculoskeletal system protects the internal organs, stores minerals, and produces blood.

[005] The primary component of the musculoskeletal system is the skeleton itself. The skeleton is a highly organized connection of bones responsible for many functions, including supporting the body against gravity, providing sites for muscle attachment, producing blood cells, protecting the organs and other soft body tissues, and permitting flexible movement.

[006] Anatomically, two types of bones can be distinguished in the skeleton: flat bones (e.g., skull bones, scapula, manible, and ileum) and long bones (e.g., tibia, femur, and humerus). The long bone is composed of two wider extremities (e.g., the epiphyses), a cylindrical tube in the middle (e.g., the midshaft or diaphysis), and a developmental zone (e.g., the metaphysis) between them. In a growing long bone, the epiphysis and the metaphysis are separated by a layer of cartilage (e.g., epiphyseal cartilage or growth plate), responsible for the longitudinal growth of the bones. The

external part of the bones is formed by a layer of calcified tissue (e.g., the cortex or compact bone). In the diaphysis, the cortex encloses the medullary cavity, the location of the hematopoietic bone marrow. Toward the metaphysis and epiphysis, the cortex becomes progressively thinner, containing a network of thin, calcified trabeculae (e.g., trabecular bone or spongy bone) and hematopoietic bone marrow. At the center of most bones is yellow marrow, which is used to store fats. Therefore, the cortical bone fulfills mainly a mechanical and protective function, and the trabecular bone fulfills a metabolic function.

[007] Bone is a balanced, dynamic system, constantly degrading and regenerating. Bone is degraded by cells called osteoclasts that remove from the center of the bone, forming the central cavity of the long bones. Osteoblasts are cells found in the osteoid tissue (e.g., bone matrix prior to calcification) and are responsible for the production of the matrix constituents of bone (e.g., collagen and ground substance). As bone matrix is produced, osteoblasts become progressively embedded and differentiate into osteocytes, or bone cells. As calcification occurs, these osteocytes then differentiate into cortical bone or trabecular bone within the calcified collagen fiber matrix. Blood vessels penetrate the newly calcified bone, bringing the blood supply that will form the hematopoietic bone marrow.

[008] Joints are formed when two bones come together and allow for bending and movement. Tough bands of connective tissue, called ligaments, surround the joints, join the two bones together, and keep the bones properly aligned. The joint capsule is lined by a synovial membrane, which produces synovial fluid for lubricating the joint. Joints may also contain fluid-filled sacs (e.g., bursa) that reduce friction in areas where skin, muscles, tendons, and ligaments rub over bones. Most joints are freely moving synovial joints; however, some joints (e.g., vertebrae) are partly movable and allow some degree of flexibility with cartilage, or menisci, between the bones, while other joints (e.g., skull sutures) do not allow movement at all.

[009] Composed of striated bundles of myosin and actin fibers, skeletal muscles have very long fiber-like cells that contract quickly, but only when stimulated by nerve cells. Muscle is attached to the bone by tough connective tissue, called tendons, and arranged in opposing, balancing groups around joints that facilitate balanced movement.

[010] Although the musculoskeletal system was designed for strength and endurance, the components of this system can become worn, injured, or inflamed. These disorders can range from mild to severe and from acute to chronic. Generally, the treatment depends on the type and severity of the disorder.

Diseases and Disorders of the Bone

[011] Several types of bone disorders occur from an imbalance of the growth and breakdown cycles of bone. The most common, osteoporosis, is a progressive decrease in the density of bones, causing them to weaken. Osteoporosis occurs in several different types and is seen more often in older women. Postmenopausal osteoporosis is generally found in women between the ages 51 and 75 and is caused by the lack of estrogen. Senile osteoporosis results not only from the imbalance between growth and breakdown but also from the calcium deficiency associated with age. Secondary osteoporosis is caused by secondary effects of another medical condition (e.g., chronic renal failure, hormonal disorders) or by drugs (e.g., barbiturates, anticonvulsants). Idiopathic juvenile osteoporosis is a rare form that occurs in children and young adults who, for no obvious reason, have weak bones. Treatment for all forms of osteoporosis is aimed at increasing bone density (e.g., estrogen intake, bisphosphonates, fluoride supplements).

[012] Paget's Disease also results from an imbalance of the growth and breakdown of bone. The turnover rate in areas affected by Paget's Disease increases tremendously; resulting in abnormal, enlarged bone that is soft and weak. Although no specific genetic pattern has been determined, Paget's Disease tends to appear in family lineages. There is no direct treatment for Paget's Disease, rather treatment is given only to alleviate pain and discomfort.

[013] Bone disorders can also result from infection. Bone can be infected through three routes: bloodstream, direct invasion, and adjacent soft tissue infections. Osteomyelitis is a bone infection usually caused by bacteria (e.g., *Staphylococcus aureus*) which results in swelling of the soft bone marrow tissue, compression of the blood vessels, and possibly death of parts of bone. Pott's disease is an infection of the vertebrae by the bacteria that cause tuberculosis (e.g., *Mycobacterium tuberculosis*, *M. bovis*, or *M. africanum*.) For acute infections, antibiotics are generally the most

effective treatment for this disease. However, if the infection is severe or chronic, surgery may also be required to remove the infected tissue and replaced with healthy bone, muscle, or skin.

[014] Most bone carcinomas are benign. The most common type of benign bone tumor, usually occurring in people aged 10 to 20, is osteochondroma. Osteochondromas are growths on the surface of a bone that protrude as hard lumps. Benign chondromas, usually occurring in people aged 10 to 30, develop in the central part of the bone. Chondroblastomas, usually occurring in people aged 10 to 20, are rare, painful tumors that grow in the ends of bones. Osteoid osteomas are very small tumors that commonly develop in the arms or legs but can occur in any bone. Giant cell tumors, usually occurring in people aged 20-40, most commonly originate in the ends of the bones and may extend into adjacent tissue. Treatment of these tumors generally involves pain management and, possibly, surgery to remove the tumor.

[015] Although rare, malignant bone tumors may be primary or metastatic. In children, most malignant bone tumors are primary; in adults, most are metastatic. The most common type of malignant primary tumor, multiple myeloma, originates in the red bone marrow cells and most commonly occurs in older people. Osteosarcoma, usually occurring in people aged 10-20, commonly occurs in or around the knee and cause pain and swelling. These tumors tend to spread to the lungs. Chondrosarcomas are slow-growing tumors composed of cancerous cartilage cells. Ewing's sarcoma, occurring most commonly in males aged 10 to 20, develop most often in arms and legs. These tumors can become large and can affect the entire length of a bone. Metastatic bone tumors most often originate from breast, lung, prostate, kidney and thyroid cancers.

[016] Treatment for bone tumors depends on the type of cancer. Most treatments are complex and involve a combination of chemotherapy, radiotherapy, and surgery. Prompt treatment is especially important for malignant bone tumors.

Diseases and Disorders of Joints, Ligaments, and Tendons

[017] The most commonly diseased tissue in the musculoskeletal system is the joint. Disorders affecting the joints and their associated components are considered connective tissue disorders because of the presence of large amounts of connective

tissue in these structures. Most of the disorders of joints involve inflammation and may be the result of an immune or autoimmune reaction.

[018] Treatment of joint disorders varies according to type and severity. Drug treatment is generally aimed at reducing inflammation. For mild inflammation and pain, drugs such as nonsteroidal anti-inflammatory drugs (NSAIDs, e.g., aspirin and ibuprofen) are commonly used. Alternative drug treatments, used in more severe cases, are corticosteroids (e.g., prednisone) and immunosuppressive drugs (e.g., methotrexate, azathioprine, and cyclophosphamide). Other treatment plans, used in conjunction with drugs, include exercise, physical therapy, and sometimes surgery.

[019] Arthritis, or inflammation of the joint, occurs in several forms. The most common form of arthritis, characterized by the degeneration of joint cartilage and adjacent bone, is osteoarthritis, or degenerative arthritis. Osteoarthritis causes the formation of rough, pitted cartilage in the joint resulting in limited joint movement, stiffness, and pain.

[020] Another form of arthritis, rheumatoid arthritis, an autoimmune disorder, is caused when the immune system attacks the tissue (e.g., ligaments, synovial membrane, bursas) that surrounds the joints. The joints, including those in the extremities, become symmetrically inflamed, resulting in swelling, pain, and eventually, destruction of the interior of the joint. Psoriatic Arthritis, occurring in people who have psoriasis, resembles rheumatoid arthritis; however, it doesn't produce the antibodies characteristic of arthritis.

[021] Other autoimmune diseases may also affect the joints and tendons. For example, systemic lupus erythematosus may result in episodes of inflammation in the joints and tendons in addition to other connective tissues and organs. Joint inflammation is common with systemic lupus erythematosus and can lead to deformity and permanent damage to the joint and its surrounding tissue; however, the bone does not erode as it does in rheumatoid arthritis.

[022] Joint disease may also result from infection. Reiter's syndrome, or reactive arthritis, is an inflammation of the joints and tendon attachments resulting from a bacterial infection originating in an area of the body other than the joints. There are two forms of Reiter's syndrome that occur more commonly in men aged 20 to 40. One occurs with sexually transmitted infections (e.g., chlamydial infection); the other

usually follows an intestinal infection (e.g., salmonellosis). Once a person is exposed to these infections, there appears to be a genetic predisposition to this type of disease.

[023] Infectious arthritis develops from an infection of the synovial fluid and tissue of a joint. Different bacteria can infect a joint, depending on the person's age. Infants and young children are most commonly infected by gram-negative bacilli, Staphylococci, and *Hemophilus influenzae*. Older children and adults are most commonly infected by gonococci, staphylococci, and streptococci. Viruses (e.g., HIV, parvoviruses, and the viruses that cause rubella, mumps, and hepatitis B) can infect joints in people of any age. The joints most commonly infected are the knee, shoulder, wrist, hip, finger, and elbow and become red, warm to the touch, swollen, and painful.

[024] Crystal deposits in the joints can cause arthritis and pain. Gout, characterized by sudden, recurring attacks of painful arthritis, is caused by the deposition of monosodium urate crystals in the joints. This accumulation generally accompanies hyperuricemia. In addition to managing the pain associated with this disorder, treatment also involves the administering of drugs to reduce the levels of uric acid in the blood by increasing the excretion of uric acid in the urine. Pseudogout, characterized by intermittent attacks of painful arthritis, is caused by the deposition of calcium pyrophosphate crystals. This disorder usually occurs in older people and causes the degeneration of the affected joints. Unfortunately, there is no effective long-term treatment available for the removals of the calcium pyrophosphate crystals. The only treatment available for pseudogout is pain management.

Diseases and Disorders of Muscles

[025] Damage to muscles can cause pain, limit control over movement, and reduce the normal range of motion. Diseases of the muscles can develop from injury, inflammation, spasms, or inheritance.

[026] Several muscle disorders are inherited. Muscular dystrophies are a group of inherited muscle disorders leading to muscle weakness. Duchenne's and Becker's muscular dystrophies are caused by different gene defects on the same gene resulting in weakness of the muscles closest to the torso. The gene for both diseases is recessive and carried on the X chromosome. Duchenne's muscular dystrophy is characterized by an almost total lack of dystrophin protein, resulting in progressive muscle loss,

including the heart muscle, and ultimately resulting in death by the age of 20. Becker's muscular dystrophy is a less severe illness characterized by production of an oversized dystrophin protein that does not function properly. Landouzy-Dejerine muscular dystrophy is transmitted by an autosomal dominant gene and results in the muscles of the face, shoulder, and legs weakening. Neither Becker's nor Landouzy-Dejerine muscular dystrophy is fatal. Currently, there is no cure for muscular dystrophies. Treatment regimens involve physical therapy and exercise to prevent the muscles from contracting permanently around the joints, and sometimes surgery to release tight, painful muscles.

[027] Myotonic myopathies are a group of inherited muscle disorders in which the muscles are not capable of fully relaxing after contraction, leading to weakness, muscle spasms, and contractures. For example, Steinert's disease is an autosomal dominant disorder producing both weakness and tight, contracted muscles, especially in the hands. Symptoms can range from mild to severe. In the most severe cases, extreme muscle weakness and many other symptoms (e.g., cataracts, irregular heartbeat, diabetes, and mental retardation) can occur, resulting in death by the age of 50.

[028] Pompe's disease is a severe, autosomal recessive, glycogen storage disease in infants where glycogen accumulates in the liver, muscles, nerves, and heart, preventing them from functioning properly. This disease is fatal by age 2; however, there are less severe forms of Pompe's disease that can affect older children and adults, causing weakness of the extremities and diminished ability to breathe deeply. Current treatments for the less severe forms of Pompe's disease and other glycogen storage diseases involve limiting exercise and diuretics to reduce the level of myoglobin released into the blood due to the muscle damage.

[029] Periodic Paralysis is another rare autosomal dominant disorder that causes sudden attacks of weakness and paralysis where the muscles do not respond to normal nerve impulses or artificial stimulation. In some families, periodic paralysis has been linked to the level of potassium in the blood with some families influenced by high levels (hyperkalemia) and some families by low levels (hypokalemia). Diet (e.g., avoidance of carbohydrate-rich food) and treatment with acetazolamide are the most common treatment to control periodic paralysis episodes.

[030] Muscle disorders may result from inflammation. For example, Polymyositis is a chronic connective tissue disease characterized by painful inflammation and disabling muscle weakness and deterioration. Although the direct cause is unknown, cancer, viruses, or autoimmune reactions may play a role. Current treatment regimens include restricting activities during periods of intense inflammation and treatment with corticosteroids or immunosuppressive drugs to improve the strength and relieve the pain and swelling associated with the disease.

[031] Although the majority of muscle disorders involve deterioration and weakening of the muscle, some disorder result in only stiffness and pain. For example, Polymyalgia rheumatica causes severe pain and stiffness in the neck, shoulders, and hips, especially in the morning and after periods of inactivity. No damage to the muscle is detected; however, erythrocyte sedimentation rate and C-reactive protein levels in the blood are high. Drug treatment involving corticosteroids are generally used to treat this disease.

[032] The discovery of new human musculoskeletal system associated polynucleotides, the polypeptides encoded by them, and the antibodies that immunospecifically bind these polypeptides, satisfies a need in the art by providing new compositions which are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of musculoskeletal system, particularly disorders of the musculoskeletal system, including, but not limited to, bone disorders (e.g., osteoporosis, osteomyelitis, Paget's disease, and sciolosis); joint disorders (e.g., osteoarthritis, rheumatoid arthritis, infectious arthritis, systemic lupus erythematosus, gout, and Reiter's syndrome); ligament, tendon, and bursa disorders (e.g., bursitis, tendinitis, and tenosynovitis); muscle disorders (e.g., muscular dystrophy, Pompe's disease, periodic paralysis, polymyalgia rheumatica, polymyositis, and Steinert's disease), neoplasms and/or cancers of musculoskeletal tissues (e.g., osteochondroma, benign chondroma, chondroblastoma, osteoid osteoma, and giant cell tumor), and/or as described under "Musculoskeletal System Disorders" below.

Summary of the Invention

[033] The present invention relates to novel musculoskeletal system related polynucleotides, the polypeptides encoded by these polynucleotides herein collectively

referred to as “musculoskeletal system antigens,” and antibodies that immunospecifically bind these polypeptides, and the use of such musculoskeletal system polynucleotides, antigens, and antibodies for detecting, treating, preventing and/or prognosing disorders of the musculoskeletal system system, including, but not limited to, the presence of cancer and cancer metastases. More specifically, isolated musculoskeletal system nucleic acid molecules are provided encoding novel musculoskeletal system polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system polynucleotides, polypeptides, and/or antibodies. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer of musculoskeletal system tissues, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The invention further relates to methods and/or compositions for inhibiting or promoting the production and/or function of the polypeptides of the invention.

Detailed Description

Tables

[034] Table 1A summarizes some of the polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) and contig nucleotide sequence identifier (SEQ ID NO:X)) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby. The first column provides a unique clone identifier, “Clone ID NO:Z”, for a cDNA plasmid related to each musculoskeletal system associated contig sequence disclosed in Table 1A. The second column provides a unique contig identifier, “Contig ID:” for each of the contig sequences disclosed in Table 1A. The third column provides the sequence identifier, “SEQ ID NO:X”, for each of the contig polynucleotide sequences disclosed in Table 1A. The fourth column, “ORF (From-To)”, provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:X that delineate

the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A as SEQ ID NO:Y (column 5). Column 6 lists residues comprising predicted epitopes contained in the polypeptides encoded by each of the preferred ORFs (SEQ ID NO:Y). Identification of potential immunogenic regions was performed according to the method of Jameson and Wolf (CABIOS, 4:181-186 (1988)); specifically, the Genetics Computer Group (GCG) implementation of this algorithm, embodied in the program PEPTIDESTRUCTURE (Wisconsin Package v10.0, Genetics Computer Group (GCG), Madison, Wisc.). This method returns a measure of the probability that a given residue is found on the surface of the protein. Regions where the antigenic index score is greater than 0.9 over at least 6 amino acids are indicated in Table 1A as "Predicted Epitopes." In particular embodiments, musculoskeletal system associated polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the predicted epitopes described in Table 1A. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. Column 7, "Tissue Distribution" shows the expression profile of tissue, cells, and/or cell line libraries which express the polynucleotides of the invention. The first number in column 7 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. Expression of these polynucleotides was not observed in the other tissues and/or cell libraries tested. For those identifier codes in which the first two letters are not "AR", the second number in column 7 (following the colon), represents the number of times a sequence corresponding to the reference polynucleotide sequence (e.g., SEQ ID NO:X) was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ³³P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal,

emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after “[array code]:” represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. Column 8, “Cytologic Band,” provides the chromosomal location of polynucleotides corresponding to SEQ ID NO:X. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Given a presumptive chromosomal location, disease locus association was determined by comparison with the Morbid Map, derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIM™. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). If the putative chromosomal location of the Query overlapped with the chromosomal location of a Morbid Map entry, an OMIM identification number is provided in Table 1A, column 9 labeled “OMIM Disease Reference(s)”. A key to the OMIM reference identification numbers is provided in Table 5.

[035] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, “Clone ID NO:Z”, for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, “SEQ ID NO:X”, for each contig sequence. The third column provides a unique contig identifier, “Contig

ID:” for each contig sequence. The fourth column, provides a BAC identifier “BAC ID NO:A” for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, “SEQ ID NO:B” for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, “Exon From-To”, provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

[036] Table 2 summarizes homology and features of some of the polypeptides of the invention. The first column provides a unique clone identifier, “Clone ID NO:Z”, corresponding to a cDNA disclosed in Table 1A. The second column provides the unique contig identifier, “Contig ID:” corresponding to contigs in Table 1A and allowing for correlation with the information in Table 1A. The third column provides the sequence identifier, “SEQ ID NO:X”, for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the row was determined. Comparisons were made between polypeptides encoded by the polynucleotides of the invention and either a non-redundant protein database (herein referred to as “NR”), or a database of protein families (herein referred to as “PFAM”) as further described below. The fifth column provides a description of PFAM/NR hits having significant matches to a polypeptide of the invention. Column six provides the accession number of the PFAM/NR hit disclosed in the fifth column. Column seven, “Score/Percent Identity”, provides a quality score or the percent identity, of the hit disclosed in column five. Columns 8 and 9, “NT From” and “NT To” respectively, delineate the polynucleotides in “SEQ ID NO:X” that encode a polypeptide having a significant match to the PFAM/NR database as disclosed in the fifth column. In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, an amino acid sequence encoded by the polynucleotides in SEQ ID NO:X as delineated in columns 8 and 9, or fragments or variants thereof.

[037] Table 3 provides polynucleotide sequences that may be disclaimed according to certain embodiments of the invention. The first column provides a unique clone

identifier, "Clone ID NO:Z", for a cDNA clone related to musculoskeletal system associated contig sequences disclosed in Table 1A. The second column provides the sequence identifier, "SEQ ID NO:X", for contig polynucleotide sequences disclosed in Table 1A. The third column provides the unique contig identifier, "Contig ID", for contigs disclosed in Table 1A. The fourth column provides a unique integer 'a' where 'a' is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, represented as "Range of a", and the fifth column provides a unique integer 'b' where 'b' is any integer between 15 and the final nucleotide of SEQ ID NO:X, represented as "Range of b", where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. For each of the polynucleotides shown as SEQ ID NO:X, the uniquely defined integers can be substituted into the general formula of a-b, and used to describe polynucleotides which may be preferably excluded from the invention. In certain embodiments, preferably excluded from the polynucleotides of the invention (including polynucleotide fragments and variants as described herein and diagnostic and/or therapeutic uses based on these polynucleotides) are at least one, two, three, four, five, ten, or more of the polynucleotide sequence(s) having the accession number(s) disclosed in the sixth column of this Table (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone).

[038] Table 4 provides a key to the tissue/cell source identifier code disclosed in Table 1A, column 7. Column 1 provides the key to the tissue/cell source identifier code disclosed in Table 1A, Column 7. Columns 2-5 provide a description of the tissue or cell source. Codes corresponding to diseased tissues are indicated in column 6 with the word "disease". The use of the word "disease" in column 6 is non-limiting. The tissue or cell source may be specific (e.g. a neoplasm), or may be disease-associated (e.g., a tissue sample from a normal portion of a diseased organ). Furthermore, tissues and/or cells lacking the "disease" designation may still be derived from sources directly or indirectly involved in a disease state or disorder, and therefore may have a

further utility in that disease state or disorder. In numerous cases where the tissue/cell source is a library, column 7 identifies the vector used to generate the library.

[039] Table 5 provides a key to the OMIMTM reference identification numbers disclosed in Table 1A, column 9. OMIM reference identification numbers (Column 1) were derived from Online Mendelian Inheritance in Man (Online Mendelian Inheritance in Man, OMIMTM. McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University (Baltimore, MD) and National Center for Biotechnology Information, National Library of Medicine, (Bethesda, MD) 2000. World Wide Web URL: <http://www.ncbi.nlm.nih.gov/omim/>). Column 2 provides diseases associated with the cytologic band disclosed in Table 1A, column 8, as determined from the Morbid Map database.

[040] Table 6 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

[041] Table 7 shows the cDNA libraries sequenced, tissue source description, vector information and ATCC designation numbers relating to these cDNA libraries.

[042] Table 8 provides a physical characterization of clones encompassed by the invention. The first column provides the unique clone identifier, "Clone ID NO:Z", for certain cDNA clones of the invention, as described in Table 1A. The second column provides the size of the cDNA insert contained in the corresponding cDNA clone.

Definitions

[043] The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

[044] In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by

electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide sequences of the present invention.

[045] As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence encoding SEQ ID NO:Y or a fragment or variant thereof, a nucleic acid sequence contained in SEQ ID NO:X (as described in column 3 of Table 1A) or the complement thereof, a cDNA sequence contained in Clone ID NO:Z (as described in column 1 of Table 1A and contained within a library deposited with the ATCC); a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B or a fragment or variant thereof; or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

[046] As used herein, a "musculoskeletal system antigen" refers collectively to any polynucleotide disclosed herein (e.g., a nucleic acid sequence contained in SEQ ID NO:X or the complement thereof, or cDNA sequence contained in Clone ID NO:Z, or a nucleotide sequence encoding the polypeptide encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B, or a nucleotide coding sequence in SEQ ID NO:B as defined in column 6 of Table 1B or the complement thereof and fragments or variants thereof as described herein) or any polypeptide disclosed herein (e.g., an amino acid sequence contained in SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, or the complement thereof, an amino acid sequence encoded by the cDNA sequence contained in Clone ID NO:Z, an amino acid sequence encoded by SEQ ID NO:B, or the complement thereof, and fragments or variants thereof as described herein). These musculoskeletal system antigens have been

determined to be predominantly expressed in musculoskeletal system tissues, including normal or diseased tissues (as shown in Table 1A column 7 and Table 4).

[047] In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown, for example, in column 1 of Table 1A, each clone is identified by a cDNA Clone ID (identifier generally referred to herein as Clone ID NO:Z). Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. Furthermore, certain clones disclosed in this application have been deposited with the ATCC on October 5, 2000, having the ATCC designation numbers PTA 2574 and PTA 2575; and on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 7 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone (Clone ID NO:Z) isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1A correlates the Clone ID NO:Z names with SEQ ID NO:X. Thus, starting with an SEQ ID NO:X, one can use Tables 1A, 6 and 7 to determine the corresponding Clone ID NO:Z, which library it came from and which ATCC deposit the library is contained in. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

[048] In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5 kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as

disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

[049] A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), the polynucleotide sequence delineated in columns 8 and 9 of Table 2 or the complement thereof, and/or cDNA sequences contained in Clone ID NO:Z (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments, or the cDNA clone within the pool of cDNA clones deposited with the ATCC, described herein) and/or the polynucleotide sequence delineated in column 6 of Table 1B or the complement thereof. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

[050] Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

[051] Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

[052] Of course, a polynucleotide which hybridizes only to polyA⁺ sequences (such as any 3' terminal polyA⁺ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

[053] The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

[054] The polypeptide of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well

known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth. Enzymol. 182:626-646 (1990); Rattan et al., Ann. N.Y. Acad. Sci. 663:48-62 (1992).)

[055] "SEQ ID NO:X" refers to a polynucleotide sequence described, for example, in Tables 1A or 2, while "SEQ ID NO:Y" refers to a polypeptide sequence described in column 5 of Table 1A. SEQ ID NO:X is identified by an integer specified in column 3 of Table 1A. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. "Clone ID NO:Z" refers to a cDNA clone described in column 1 of Table 1A.

[056] "A polypeptide having biological activity" refers to a polypeptide exhibiting activity similar to, but not necessarily identical to, an activity of a polypeptide of the

present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

[057] Table 1A summarizes some of the musculoskeletal system associated polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and clones (Clone ID NO:Z) and further summarizes certain characteristics of these polynucleotides and the polypeptides encoded thereby.

Polynucleotides and Polypeptides

TABLE 1A

Clone ID NO: Z	Contig ID:	SEQ ID NO: X	ORF (From-To)	AA SEQ ID NO: Y	Predicted Epitopes	Tissue Distribution Library code: count (see Table IV for Library Codes)	Cytologic Band	OMIM Disease Reference(s):
HANGA63	927404	11	168 - 254	1034		S0318: 1 and S0316: 1.		
HANGA69	718174	12	86 - 268	1035	Ser-21 to His-27, Ser-33 to Ser-39.	S0318: 1 and S0316: 1.		
HANGA85	746265	13	192 - 317	1036		S0318: 1 and S0316: 1.		
HANGA92	791182	14	24 - 146	1037	Glu-8 to Phe-14, Ser-20 to Gly-27.	S0318: 1 and S0316: 1.		
HANGC05	674059	15	2 - 157	1038	Met-2 to His-18, Phe-21 to Thr-27, Lys-43 to Lys-49.	S0318: 1 and S0316: 1.		
HANGC07	952586	16	95 - 226	1039	Ser-28 to Thr-44.	S0318: 1 and S0316: 1.		
HANGC14	952581	17	5 - 151	1040		S0318: 1 and S0316: 1.		
HANGC30	966430	18	16 - 192	1041	Arg-10 to Ser-17, Tyr-37 to His-43.	S0318: 1 and S0316: 1.		
HANGC33	702072	19	49 - 144	1042	Glu-27 to Pro-32.	S0318: 1 and S0316: 1.		
HANGC59	653577	20	72 - 179	1043	Ser-9 to Lys-36.	S0318: 1 and S0316: 1.		
HANGC84	715991	21	106 - 279	1044	Asp-20 to Asn-26.	S0318: 1 and S0316: 1.		
HANGF36	952583	22	126 - 206	1045	Thr-1 to Lys-8.	S0318: 2 and S0316: 1.		
HANGF49	722635	23	34 - 126	1046		S0318: 1 and S0316: 1.		
HANGG22	848727	24	17 - 247	1047	Pro-71 to Thr-77.	S0316: 2		
HANGH48	718759	25	89 - 232	1048	Thr-4 to Leu-11, Gln-27 to Leu-34, Gln-41 to Arg-47.	S0318: 1 and S0316: 1.		
HANGH53	727914	26	75 - 269	1049	Asn-19 to Glu-25, Val-45 to Asn-54.	S0318: 1 and S0316: 1.		

HANGH58	811987	27	34 - 228	1050			S0318: 1 and S0316: 1.		
HANGH66	661513	28	2 - 220	1051	Tyr-1 to Lys-6, Thr-30 to His-36.		S0318: 1 and S0316: 1.		
HANKD09	625167	29	188 - 298	1052			S0318: 1 and S0316: 1.		
HANKD47	719963	30	227 - 370	1053	Ala-2 to Ser-9.		S0318: 1 and S0316: 1.		
HANKD83	963964	31	130 - 312	1054	Arg-21 to Ile-30, Lys-42 to Lys-48.		S0318: 1 and S0316: 1.		
HANKG78	710760	32	3 - 176	1055			S0318: 1, S0316: 1 and L0777: 1.		
HANKG90	746282	33	133 - 366	1056			S0318: 1 and S0316: 1.		
HANKH48	721340	34	159 - 356	1057	Ser-32 to Asn-41, Ser-44 to Ser-51.		S0318: 2 and S0316: 1.		
HANKH56	733063	35	202 - 318	1058	His-13 to Pro-18.		S0318: 1 and S0316: 1.		
HAOAA57	955693	36	139 - 2	1059			S0312: 2 and S0314: 1.		
HAOAA78	756979	37	384 - 539	1060			S0312: 3 and S0314: 2.		
HAOAA90	919249	38	82 - 279	1061	Leu-14 to Thr-20, Glu-40 to Asp-52.		S0314: 2		
HAOAC05	932017	39	118 - 312	1062	Arg-34 to Thr-43, Glu-53 to Arg-58.		S0314: 2 and S0312: 1.		
HAOAD47	864899	40	235 - 384	1063	Met-1 to Thr-12.		S0314: 2		
HAOAE53	964029	41	112 - 381	1064	Arg-1 to Leu-6, Gly-29 to Met-36.		S0312: 1 and S0314: 1.		
HAOAE56	767915	42	1 - 234	1065			S0312: 1 and S0314: 1.		
HAOAE60	657909	43	2 - 238	1066	Thr-8 to Gln-16, Pro-58 to Pro-68.		S0312: 1 and S0314: 1.		
HAOAF68	752788	44	336 - 581	1067			L0731: 2, S0312: 1 and S0314: 1.		
HAOAH38	705946	45	239 - 337	1068			S0312: 1 and S0314: 1.		

HAOMA13	915881	46	94 - 288	1069	Arg-19 to Ser-26, Val-36 to Asn-44, Gly-52 to Thr-59.	S0312: 2		
HAOMB64	960293	47	138 - 386	1070		S0003: 2 and S0312: 1.		
HAOMC21	670518	48	52 - 237	1071	Ala-11 to Glu-22, Arg-38 to Ser-47.	S0312: 2		
HAOMD90	788658	49	87 - 242	1072	Pro-11 to Ser-24, Ser-35 to Pro-41.	S0312: 2		
HAOME45	705947	50	56 - 280	1073	Gln-1 to Gln-11, Arg-24 to Ile-46, Arg-50 to Cys-61.	S0312: 2		
HBCGA72	756953	51	1 - 150	1074	Pro-5 to Pro-20.	S0334: 2		
HBCKB24	676825	52	239 - 412	1075		S0336: 2		
HBCKB82	779562	53	232 - 516	1076		S0336: 2	12q21	217300, 600808
HBCKE22	674041	54	16 - 159	1077		S0336: 2, L0794: 2, L0523: 1, L0607: 1 and L0559: 1.		
HBCKE78	746109	55	321 - 659	1078		S0336: 1, S0250: 1, L0766: 1 and L0362: 1.		
HBFCMC73	764150	56	200 - 334	1079		S0362: 1 and H0529: 1.		
HBSAK76	506666	57	51 - 176	1080	Tyr-6 to Lys-16.	H0381: 2		
HBSAL69	573004	58	67 - 402	1081	Gly-3 to Tyr-8, Gln-11 to Thr-17.	H0381: 1 and H0419: 1.		
HBSAL80	506580	59	1 - 378	1082	Pro-3 to Phe-10, His-29 to Leu-34, Gln-46 to Val-54, Val-70 to Gln-76.	H0381: 1 and H0419: 1.		
HBSAM46	526732	60	202 - 345	1083		H0381: 2		

HBSAM48	727635	61	26 - 298	1084			H0381: 1 and S0028: 1.		
HBSAP02	920648	62	141 - 338	1085			H0381: 1 and H0041: 1.		
HBSAP73	764589	63	3 - 227	1086		Thr-22 to Arg-27, His-64 to Thr-73.	S0028: 2 and H0381: 1.		
HBSAQ64	530344	64	192 - 308	1087			H0381: 1 and S0003: 1.		
HBSDDB50	571365	65	2 - 367	1088		Arg-56 to Glu-76.	AR061: 2, AR089: 0 H0419: 2		
HBSDDB63	745211	66	146 - 343	1089		Pro-18 to Pro-45, Leu-49 to Arg-66.	H0419: 2		
HBSDDD91	775313	67	42 - 149	1090			H0419: 2		
HCDAA94	661278	68	3 - 167	1091			H0251: 5		
HCDAB17	530726	69	187 - 321	1092			H0251: 2, L0586: 1 and L0589: 1.		
HCDAE77	533925	70	60 - 251	1093		Lys-34 to Glu-43, Val-59 to Leu-64.	H0251: 4		
HCDAF27	592244	71	48 - 200	1094		Ser-3 to Pro-11.	H0251: 5		
HCDAF29	533812	72	80 - 235	1095			H0251: 3		
HCDAF54	530529	73	156 - 434	1096			H0251: 2		
HCDAG92	724693	74	66 - 194	1097			H0251: 7		
HCDAG95	533871	75	102 - 296	1098		Cys-32 to Ile-44.	H0251: 5		
HCDAH34	533870	76	45 - 248	1099		Glu-1 to Gln-10.	H0251: 4		
HCDAJ67	925362	77	18 - 185	1100			H0251: 3		
HCDAK93	523648	78	77 - 199	1101			H0251: 2		
HCDAK96	960047	79	3 - 362	1102		Asp-4 to Ser-9.	H0251: 12		
HCDAM34	523607	80	1 - 231	1103		Phe-30 to Arg-37, Glu-45 to His-50.	H0251: 3		
HCDAO32	530006	81	192 - 314	1104			H0251: 2		

HC DAT56	533881	82	388 - 558	1105		H0251: 3, L0766: 1 and L0756: 1.		
HC DBO13	709590	83	41 - 238	1106		H0251: 10		
HC DBR37	968501	84	80 - 331	1107		H0251: 4	12q14	123829, 147570, 181430, 252940, 264700, 600808, 601284, 601769, 601769, 602116
HC DBR39	921893	85	2 - 361	1108	Ala-1 to Arg-9, Arg-15 to Lys-29, Ala-47 to Ser-59, Gly-81 to Thr-92.	H0251: 10 and S0001: 1.		
HC DBU77	661272	86	53 - 172	1109		H0251: 3		
HC DBW51	556469	87	48 - 293	1110		H0251: 5		
HC DBW61	960044	88	32 - 115	1111		H0251: 2 and L0756: 1.		
HC DBX78	847580	89	63 - 257	1112		H0251: 3		
HC DCB84	670159	90	3 - 125	1113	Lys-1 to Asp-6.	H0251: 3		
HC DCE48	529893	91	89 - 205	1114	Asn-1 to His-9, Thr-11 to Lys-19.	H0251: 2		
HC DCE62	523582	92	21 - 161	1115		H0251: 3		
HC DCF11	967768	93	159 - 248	1116		H0251: 2		
HC DCK07	865908	94	2 - 148	1117	Leu-22 to Glu-27.	H0251: 2	7q22.1	120160, 120160, 120160, 120160, 126650, 126650
HC DCK91	592465	95	18 - 176	1118	Arg-13 to Ser-21, Ser-40 to Lys-46.	H0251: 3		
HC DCR26	960048	96	191 - 319	1119		H0251: 3		

HCDCX68	529778	97	30 - 104	1120			H0251: 2		
HCDCY13	921702	98	2 - 73	1121			H0251: 2		
HCDDB52	847581	99	100 - 267	1122			H0251: 3		
HCDDB62	529890	100	43 - 177	1123			H0251: 2		
HCDDI61	529937	101	3 - 83	1124			H0251: 2		
HCDDU07	954177	102	3 - 173	1125			H0251: 2		
HCDDV90	847575	103	20 - 157	1126		Pro-36 to Lys-46.	H0251: 3		
HCDDY57	556465	104	244 - 363	1127		Arg-12 to Cys-22.	H0251: 4		
HCDDZ09	523605	105	160 - 396	1128			H0251: 2		
HCDDZ44	863388	106	3 - 458	1129			H0251: 4		
HCDEB49	847572	107	1 - 144	1130		Tyr-1 to Gln-16, Asn-21 to Ala-27.	H0251: 2		
HCDEB78	921710	108	21 - 119	1131			H0251: 2		
HCDEG67	531239	109	257 - 355	1132			H0251: 2		
HCDEG95	533879	110	123 - 287	1133			H0251: 5		
HCDER16	667338	111	85 - 270	1134		Asn-36 to Cys-41.	H0251: 1 and S0028: 1.		
HCDER29	523506	112	2 - 211	1135			H0251: 3		
HCDET89	524045	113	157 - 342	1136			H0251: 3		
HFIAB89	848927	114	1 - 48	1137			S0192: 2		
HFIAB93	713799	115	317 - 463	1138			S0192: 2		
HFIAE82	779898	116	2 - 124	1139		Pro-1 to Leu-9.	S0192: 1 and S0194: 1.		
HFIAH10	964652	117	93 - 236	1140		Asn-22 to Thr-28.	S0192: 2		
HFIAI07	952884	118	21 - 188	1141			S0192: 2 and L0748: 1.		
HFIAP31	697775	119	3 - 203	1142		Ser-22 to Ala-28, Arg-52 to Arg-66.	S0192: 4		
HFIAP89	587844	120	145 - 348	1143			S0192: 3		
HFIAP91	925831	121	486 - 214	1144			S0192: 2		
HFIAPV83	780358	122	146 - 36	1145		Lys-24 to Leu-32.	S0192: 2		

HFIAZ63	966761	123	137 - 355	1146	Thr-17 to Ser-22.	S0192: 16 and L0809: 1.		
HFIBI48	587871	124	1 - 210	1147	Arg-1 to Ser-6, Leu-34 to Asp-42.	S0192: 5		
HFICA06	934675	125	2 - 244	1148		S0192: 2		
HFICE40	587918	126	143 - 310	1149		S0192: 5		
HFICF01	916103	127	111 - 212	1150		S0192: 2		
HFICI52	522239	128	2 - 568	1151	Arg-1 to Arg-8.	S0028: 1 and S0192: 1. 1q31-q32	114208, 114208, 119300, 120620, 120620, 120920, 134370, 134370, 134370, 134580, 145001, 145260, 150292, 150310, 150310, 179820, 191045, 208250, 226450, 600105, 600759, 600995, 601494, 601652, 601975	
HFICM95	587875	129	148 - 261	1152	Pro-18 to Asn-23.	S0192: 2		
HFICZ77	934192	130	1 - 141	1153	Pro-1 to Arg-11.	S0192: 2		
HFIDB12	968922	131	288 - 509	1154	Ala-2 to Lys-7, Pro-23 to His-29.	S0192: 2		
HFIDL94	964316	132	122 - 325	1155	Asn-1 to Ser-11.	S0192: 4		
HFIDM69	926894	133	336 - 485	1156		S0192: 4		
HFIDN81	959050	134	454 - 302	1157		S0192: 3		
HFIEC13	883185	135	1 - 525	1158	Glu-1 to Arg-13.	AR061: 168, AR089:		

								145 S0192: 2			
HFIHF04	926824	136	2 - 112	1159		Pro-16 to Val-26.		S0192: 3			
HFIHF79	855196	137	449 - 640	1160				S0192: 55			
HFIHB16	661971	138	1 - 132	1161		Leu-21 to Gly-26, Leu-29 to Glu-35.		S0192: 3 and S0194: 1.			
HFIHD91	702324	139	582 - 734	1162		Asp-10 to Lys-18, Arg-37 to Cys-42, Gln-46 to Asn-51.		S0194: 2 and L0740: 1.			
HFIHE47	857988	140	385 - 1659	1163		Pro-1 to Gly-6, Phe-31 to Thr-36, Gln-66 to Leu-75, Leu-83 to Pro-91.		AR089: 17, AR061: 17 S0250: 1, L0439: 1 and S0194: 1.			
HFIHF63	944246	141	2 - 610	1164				AR061: 1, AR089: 1 L0747: 3, S0250: 1, L0777: 1, L0731: 1, L0758: 1 and S0194: 1.			
	973023	1010	895 - 530	2033		Pro-6 to Cys-13, Pro-15 to Leu-20, Pro-47 to Gly-59, Asn-82 to Ser-88.					
HFIHJ60	740280	142	34 - 177	1165		Lys-39 to Tyr-45.		S0194: 2			
HFIHJ85	707899	143	212 - 385	1166		Met-1 to Thr-7, Gly-10 to Cys-21, Ile-25 to Trp-30, Pro-41 to Glu-49.		S0276: 4 and S0194: 1.			
HFIHL29	690546	144	46 - 156	1167				S0022: 1 and S0194: 1.			
HFIHS76	769952	145	246 - 404	1168		Asn-16 to Arg-21.		S0194: 2			

HFIHZ33	588058	146	279 - 455	1169	Arg-7 to Cys-14, Glu-26 to Ser-32.	L2245: 1, L0731: 1, L0604: 1, S0194: 1 and S0276: 1.		
HFIHZ51	725587	147	1 - 201	1170	Glu-47 to Lys-53.	S0194: 2		
HFIIB73	669594	148	262 - 441	1171		S0194: 1 and S0276: 1.		
HFIIS21	670765	149	141 - 332	1172		S0206: 1 and S0194: 1.		
HFIUF34	703972	150	1 - 144	1173	Glu-1 to Gln-16, Ser-42 to Gly-48.	S0194: 1 and S0276: 1.		
HFIIX48	934328	151	239 - 466	1174	Thr-1 to Asp-8.	S0196: 3 and S0242: 2.		
HFIIZ24	677144	152	28 - 426	1175		S0196: 2		
HFIUE17	855119	153	182 - 307	1176		S0242: 7, S0196: 2 and L0792: 1.		
HFIUH54	929787	154	246 - 443	1177		S0196: 16 and S0242: 13.		
HFIUI66	746397	155	2 - 103	1178	Thr-7 to Asn-12, Ser-21 to Trp-28.	S0242: 1 and S0196: 1.		
HFIUJ95	735969	156	48 - 167	1179		S0196: 2		
HFIUM59	724249	157	122 - 244	1180		S0196: 2		
HFIUO63	691921	158	161 - 334	1181	Trp-10 to Pro-15.	L0754: 1, S0242: 1 and S0196: 1.		
HFIUP04	582296	159	2 - 88	1182		S0196: 2	1p22	170995, 191540, 274270, 274270, 600309, 601414, 602094
HFIIVB03	924021	160	55 - 195	1183	Ser-5 to Lys-13, Arg-39 to Tyr-47.	S0196: 3 and S0242: 1.		
HFIIVB25	678022	161	20 - 130	1184		S0196: 2		
HFIIVB62	741665	162	91 - 255	1185	Gln-38 to Arg-48.	S0242: 1 and S0196: 1.		

HFIVQ02	919802	163	214 - 453	1186	Glu-46 to Arg-53.	S0242: 1 and S0196: 1.		
HFIXA30	692637	164	142 - 243	1187		L0759: 2, S0242: 2, L0766: 1 and L0663: 1.		
HFIXC30	692635	165	37 - 282	1188		S0242: 2		
HFIXC44	839536	166	369 - 554	1189	His-1 to Asp-9.	L0439: 6, S0242: 2 and L0438: 1.		
HFIXC49	722886	167	2 - 172	1190	Glu-6 to Leu-17, Ser-36 to Gly-41.	S0242: 2		
HFIXK83	767156	168	170 - 364	1191		S0242: 2		
HFIXK94	943717	169	58 - 417	1192		AR089: 2, AR061: 1 S0242: 1 and S0196: 1.		
HFIXM11	966714	170	3 - 95	1193	Phe-5 to Glu-13.	S0242: 2		
HFIXO03	923735	171	269 - 373	1194		S0242: 2		
HFIXV93	597031	172	115 - 297	1195		S0242: 1 and S0196: 1.		
HFIYX13	656812	173	148 - 258	1196		S0242: 2		
HFIYX57	734580	174	143 - 280	1197		S0242: 2		
HFIYX80	965077	175	1 - 174	1198	Asn-45 to Gly-57.	S0242: 2		
HFIYA86	757155	176	192 - 356	1199		S0242: 1 and S0196: 1.		
HFIYB24	952847	177	107 - 304	1200	Asn-14 to Asn-19.	S0242: 2		
HFIYB40	964251	178	101 - 283	1201	Pro-6 to Arg-13, Gly-46 to Arg-52.	S0242: 4 and S0196: 1.		
HFIYK01	916125	179	1 - 123	1202	Gly-1 to Gln-6.	S0242: 2		
HFIYL01	919416	180	2 - 277	1203	Arg-17 to Pro-23, Asp-52 to Lys-74.	S0242: 1 and S0276: 1.		
HFIYO14	657598	181	2 - 145	1204		S0242: 2 and L0779: 1.		
HFIYP02	919501	182	1 - 162	1205	Pro-8 to Arg-16, Pro-34 to Leu-46.	S0242: 3		
HFIYV01	916064	183	264 - 425	1206	Gly-1 to Gly-12.	S0011: 1 and S0242: 1.		

HFIYV03	923755	184	173 - 298	1207	Lys-31 to Asn-38.	S0242: 2		
HFIYV59	861487	185	25 - 255	1208		S0242: 2		
HFIYW08	958978	186	7 - 198	1209	Gln-47 to Lys-52.	S0242: 2		
HFIYZ13	656795	187	1 - 321	1210	Gln-32 to Arg-40, Ser-49 to Ser-59, Asp-71 to Asn-88.	S0242: 2		
HFIZF95	795734	188	52 - 204	1211		S0242: 2 and L0754: 1.		
HFIZG93	928170	189	239 - 406	1212		S0242: 4		
HFIZH29	953895	190	252 - 392	1213	Lys-1 to Thr-9, Thr-15 to Gly-23.	H0124: 1 and S0242: 1.		
HFIZM92	791267	191	403 - 573	1214		L0754: 2, S0242: 1 and S0194: 1.		
HFOXA79	774901	192	74 - 250	1215	Gly-25 to Trp-30, Gly-36 to Pro-47.	S0276: 2		
HFOX85	752957	193	195 - 374	1216		S0276: 2		
HFOXC25	677995	194	64 - 186	1217	Thr-7 to Gly-14, His-30 to Pro-35.	S0276: 3		
HFOXC35	638311	195	2 - 358	1218	Pro-1 to Glu-12.	S0276: 2		
HFOX83	587955	196	185 - 283	1219	Lys-13 to Gly-29.	S0276: 3		
HFOX103	923772	197	160 - 321	1220		S0276: 2		
HFOX54	587974	198	53 - 211	1221		S0276: 2		
HFOXN89	587984	199	76 - 2	1222		S0276: 2		
HFOX024	733377	200	247 - 414	1223	Gly-1 to Tyr-8.	S0214: 1 and S0276: 1.		
HFOX28	587994	201	166 - 324	1224	Phe-4 to Ser-10.	S0276: 2		
HFOX67	806488	202	3 - 257	1225	Pro-21 to Asn-30.	S0276: 3		
HFOX81	588052	203	144 - 383	1226	Ala-5 to Phe-14, His-45 to Lys-58.	S0276: 2		
HFOXU83	887781	204	1 - 267	1227		AR051: 17, AR054: 8,		

									AR050: 5 S0276: 3			
HFOXU92	588057	205	77 - 3	1228				Ile-2 to Ala-16.	S0276: 2			
HFOXV15	964296	206	159 - 335	1229					S0276: 2			
HFOXV80	771290	207	1 - 426	1230				Leu-3 to His-14, Pro-19 to Thr-49, Ala-54 to Gly-59, Leu-77 to Gly-82, Gln-87 to Ala-100.	S0340: 1 and S0276: 1.			
HFOYI36	935532	208	2 - 178	1231				Val-3 to Leu-10, Asn-18 to Lys-37, Pro-45 to Val-51.	S0192: 1 and S0276: 1.			
HFOYL77	494844	209	9 - 185	1232					S0276: 2			
HMUBM26	908912	210	2 - 565	1233				Ser-1 to Ser-9, His-28 to Glu-35, Phe-71 to Asn-76, Val-83 to Gly-96, Phe-99 to Asn-104, Lys-109 to Ser-116, Cys-120 to Cys-129, His-140 to Glu-150, Pro-161 to Trp-170.	AR089: 20, AR061: 8 H0529: 1 and S0032: 1.			
HMUBX25	678004	211	1 - 261	1234				Ser-1 to Ala-8, Pro-65 to Leu-70.	H0529: 2			
HMUBY88	740311	212	1 - 372	1235				Tyr-44 to Pro-55, Thr-72 to Arg-77, Phe-92 to Lys-110.	H0529: 2			
HOAAB15	575254	213	1 - 114	1236				Ser-1 to Gly-7,	H0529: 2			

							Gly-18 to Ala-23, Lys-25 to Val-36.				
HOAAB42	530605	214	3 - 209	1237					H0252: 2	12p11	
HOAAB56	507839	215	2 - 190	1238			Phe-38 to Gly-50.		H0252: 3		
HOAAC31	693597	216	3 - 95	1239			Thr-3 to Gly-10.		L0766: 3 and H0252: 2.		
HOAAD05	932756	217	560 - 126	1240					H0252: 2, L0753: 2, L0455: 1, L0770: 1, L0779: 1 and L0731: 1.		
HOAAD52	859628	218	140 - 331	1241			Met-1 to Leu-11, Ser-22 to Lys-29.		H0252: 3		
HOAAE10	968532	219	89 - 208	1242					H0252: 2		
HOAAE45	530602	220	106 - 330	1243			Gly-34 to Asn-51.		H0252: 2		
HOAAE49	859630	221	78 - 302	1244			His-6 to Lys-11, Glu-27 to Lys-38.		H0041: 1 and H0252: 1.		
HOAAE73	960631	222	3 - 161	1245			Arg-13 to Cys-30, Val-37 to Phe-47.		H0252: 3		
HOAAF18	530600	223	156 - 347	1246			Thr-1 to Ala-10.		H0252: 2		
HOAAH10	968368	224	200 - 454	1247			Gly-53 to Asp-64, Pro-72 to Arg-85.		H0252: 2, L0748: 2, L0518: 1 and L0759: 1.		
HOAAI05	932537	225	87 - 251	1248			Asp-32 to Ser-45.		H0252: 2		
HOAAJ23	531389	226	28 - 135	1249			Lys-1 to Asp-8, Lys-12 to Lys-28.		H0252: 2		
HOAAK90	527490	227	2 - 178	1250					H0252: 2		
HOAAM08	960060	228	25 - 201	1251			Ala-14 to Thr-36.		H0252: 2		
HOAAR14	526530	229	2 - 202	1252			Arg-17 to Lys-22, Thr-39 to Lys-54.		H0252: 2		
HOAAV23	527489	230	1 - 306	1253					H0252: 2		

HOAAW21	527487	231	193 - 309	1254	Val-22 to Gly-28, Gly-31 to Gly-36.	H0252: 2		
HOAAZ61	531065	232	31 - 333	1255	Gln-4 to Cys-12.	H0252: 2		
HOABA20	932539	233	23 - 118	1256		H0252: 2		
HOABA93	792929	234	78 - 146	1257		H0252: 2		
HOABD58	738359	235	3 - 110	1258		H0252: 2		
HOABP66	507175	236	86 - 253	1259	Lys-39 to Gly-44.	H0252: 2		
HOABP69	531049	237	2 - 76	1260		H0252: 2		
HOABR40	531051	238	245 - 358	1261	Gly-1 to Asp-8.	H0252: 2		
HOEAK21	954961	239	2 - 280	1262		S0126: 4		
HOEAY14	659258	240	25 - 132	1263		S0126: 3, L0520: 1 and L0749: 1.		
HOEBL44	715851	241	69 - 272	1264		S0126: 2		
HOEBO31	693689	242	2 - 103	1265		S0126: 2		
HOEBP01	916957	243	3 - 470	1266	Lys-11 to Asp-17, Tyr-24 to Asp-29, Leu-50 to Ser-64, Ala-76 to Phe-81, Arg-132 to Ser-137.	L0439: 3 and S0126: 2.		
HOECN79	723113	244	88 - 237	1267		S0126: 9, H0658: 1 and L0602: 1.		
HOECY54	506692	245	31 - 342	1268	Lys-28 to Glu-33, Lys-38 to Thr-54, Pro-61 to Ser-70.	S0126: 2		
HOEDD40	572900	246	86 - 346	1269	Pro-8 to Glu-20, Arg-32 to Gly-41, Ser-49 to Arg-61.	S0126: 2		
HOEDD83	578934	247	34 - 267	1270		S0126: 2		

HOEDK10	915054	248	1 - 276	1271	Gly-10 to Asp-15, Gly-31 to Gly-38, Arg-41 to Asp-55.	S0126: 9		
HOEDT31	826009	249	148 - 474	1272		S0126: 3		
HOEDU54	506576	250	391 - 513	1273	Asn-9 to Pro-15.	S0126: 5 and L0661: 1.		
HOEDU68	713695	251	32 - 169	1274	Arg-28 to Tyr-36, Pro-40 to Ser-46.	S0126: 2		
HOEEB63	745039	252	2 - 310	1275	Gly-6 to Gly-12, Ala-14 to Pro-19.	S0126: 2		
HOEEC02	919822	253	143 - 235	1276	Arg-1 to Gly-14.	S0126: 4		
HOEE045	717754	254	62 - 238	1277		S0126: 2		
HOEEQ17	663719	255	173 - 298	1278	Asp-20 to Ala-25.	S0126: 5		
HOEFG22	744340	256	97 - 285	1279	Ser-13 to Ala-18.	S0126: 1 and S3012: 1.		
HOEFL91	790134	257	1 - 135	1280		S0126: 5, L0022: 1, L0752: 1 and L0581: 1.		
HOEFN92	698444	258	170 - 325	1281	Lys-26 to Gly-31, Pro-35 to Asn-45.	S0126: 2		
HOEFS83	615154	259	2 - 220	1282		S0126: 2		
HOEJE18	666349	260	90 - 278	1283		S0126: 2		
HOEJG04	859251	261	3 - 482	1284	Asp-76 to Ile-84, Thr-122 to Trp-139.	AR089: 1, AR061: 0 S0126: 2, S0028: 1 and : 1.		
HOEJW84	859225	262	195 - 425	1285		S0126: 2 and L0748: 2.		
HOEKH88	924112	263	2 - 172	1286	Pro-17 to Lys-23, Leu-31 to Ser-36.	S0126: 3 and S0028: 1.		
HOEKP01	918873	264	3 - 329	1287	Gln-1 to Arg-13, Pro-27 to Pro-41.	S0126: 3		
HOEKP79	963337	265	309 - 467	1288		S0126: 5		

HOEME76	974069	266	6 - 488	1289	Lys-8 to Ser-16, Tyr-81 to Ile-94, Ser-97 to Asp-111.	S0126: 2		
HOEMK02	918364	267	3 - 89	1290		S0126: 2		
HOEMQ65	922789	268	132 - 323	1291		S0126: 2		
HOEOE25	907806	269	2 - 625	1292	Lys-95 to Asp-103, Pro-108 to Leu-115, Lys-150 to Leu-158, Leu-162 to Trp-167, Leu-177 to Lys-186, Glu-201 to Gln-208.	L0766: 4, L0517: 2, S0126: 2, L0794: 1 and L0366: 1.		
HOHAA14	468867	270	185 - 385	1293		S0250: 2		
HOHAB04	665381	271	183 - 284	1294		S0250: 2		
HOHAB21	670814	272	3 - 158	1295	Ser-10 to Phe-16, Asn-22 to Asn-27.	S0250: 2		
HOHAE68	781448	273	20 - 286	1296		S0250: 2		
HOHAM36	782043	274	1 - 138	1297	Gly-27 to Asp-35.	S0250: 2, L0598: 1, L0766: 1 and L0745: 1.		
HOHBE48	588317	275	77 - 364	1298	Lys-1 to Ser-6, Thr-9 to Lys-22, Ser-65 to Lys-73.	S0250: 2		
HOHBF30	859046	276	153 - 518	1299	Leu-43 to Pro-49, Asp-108 to Asp-120.	S0250: 2		
HOHBL11	966720	277	23 - 280	1300	Gln-4 to Gly-13, Arg-21 to Glu-29.	S0250: 2		
HOHBL32	588329	278	273 - 461	1301	Asn-43 to His-52.	S0250: 2		
HOHBO79	588271	279	245 - 442	1302	Pro-1 to Gly-17, Gln-23 to Gly-34.	S0250: 2		

HOHBW86	784723	280	111 - 278	1303	Trp-8 to Gly-17, Glu-25 to Gly-30.	S0250: 1 and S0028: 1.		
HOHBX75	669536	281	3 - 497	1304	Gln-13 to Gly-24, Asn-63 to Ala-70.	S0250: 2		
HOHBY75	840109	282	191 - 304	1305		S0250: 2 and L0465: 1.		
HOHCH04	859047	283	3 - 581	1306	Cys-1 to Pro-8.	S0250: 2		
HOHCI05	935123	284	54 - 155	1307		S0250: 2		
HOHCM38	709295	285	114 - 227	1308	Tyr-31 to Phe-38.	S0250: 2		
HOHCM90	703734	286	3 - 152	1309		S0250: 2		
HOHCO85	751299	287	93 - 260	1310	Pro-49 to Lys-56.	S0250: 2	6q12-q13	203310
HOHCP35	656516	288	155 - 295	1311	Tyr-8 to Glu-15, Thr-26 to Lys-34.	S0250: 2		
HOHCQ76	825236	289	157 - 330	1312		S0250: 2		
HOHCQ77	661480	290	2 - 115	1313		S0250: 2		
HOHCV83	735685	291	8 - 241	1314		S0250: 2		
HOHCW02	919142	292	159 - 284	1315		S0250: 2		
HOHDB11	966413	293	3 - 440	1316		S0250: 2, L0740: 2 and L0777: 1.		
HOHDB32	698781	294	1 - 162	1317	Pro-21 to Asn-32, Gln-37 to Thr-54.	S0250: 3		
HOHDD23	675616	295	266 - 412	1318		S0250: 2		
HOHDF40	710748	296	2 - 337	1319	Phe-3 to Trp-10, Asn-27 to Asn-40, Ser-43 to Lys-48, Thr-52 to Ser-61, Met-72 to Asp-77, Leu-82 to Thr-89.	S0250: 2 and L0777: 1.		
HOHDF53	727620	297	219 - 344	1320		S0250: 2		

HOHDI48	966379	298	3 - 131	1321	Ser-11 to Lys-20.	S0250: 2		
HOHDY85	764155	299	189 - 347	1322	Gln-1 to Gln-17.	S0250: 2		
HOHDZ61	741382	300	41 - 175	1323		S0250: 2		
HOHEA19	668208	301	112 - 273	1324		S0250: 6		
HOHEC41	712037	302	27 - 470	1325	Asp-1 to Asp-11, Glu-24 to Lys-29.	S0250: 2, L0807: 1 and L0591: 1.		
HOHEN50	662365	303	2 - 163	1326		S0250: 2		
HOSAB04	531565	304	82 - 324	1327	Gln-34 to Lys-42, Ser-73 to Arg-81.	S0003: 2		
HOSAR25	509226	305	2 - 208	1328		S0003: 2		
HOSBR08	925430	306	3 - 107	1329		S0003: 2		
HOSBU17	667195	307	365 - 505	1330	Leu-25 to Arg-30, Lys-34 to Gln-39.	S0003: 2 and L0589: 1.		
HOSBU81	508735	308	43 - 168	1331	Asp-28 to Thr-34.	S0003: 2		
HOSBV22	780092	309	1 - 204	1332	Trp-1 to Asp-7, Glu-14 to Trp-28.	S0003: 2, L0775: 2, L0770: 1, L0804: 1 and L0659: 1.		
HOSBW16	933016	310	6 - 155	1333		S0003: 2		
HOSCG51	967584	311	129 - 422	1334		S0003: 1 and S0122: 1.		
HOSCM15	921336	312	126 - 353	1335	Ser-2 to Gln-7, Tyr-40 to Thr-47.	S0003: 2		
HOSCZ35	707379	313	23 - 256	1336		S0003: 2 and S0126: 1. 5q22	175100, 175100, 175100, 175100, 175100, 175100	
HOSDE63	580959	314	3 - 122	1337		S0003: 1, S0027: 1 and S0032: 1.		
HOSDG51	523872	315	23 - 148	1338		S0003: 2		
HOSDN27	530459	316	2 - 154	1339	Ile-1 to Thr-12.	S0003: 2		

HOSEB61	741812	317	359 - 601	1340	Gly-8 to Ser-17, Ala-50 to Asp-62.	S0003: 1, S0214: 1 and L0756: 1.		
HOSEM84	831049	318	160 - 327	1341	Pro-31 to Gly-38, Leu-49 to Arg-56.	S0214: 2	2	
HOSFO57	736034	319	85 - 234	1342		S0214: 2		
HOSFV63	873010	320	14 - 112	1343		S0214: 2	10	
HOSFY79	774052	321	214 - 336	1344	Gly-1 to Gln-10, Asn-20 to Gly-25, Glu-28 to Arg-35.	S0214: 2		
HOSFZ39	705351	322	180 - 344	1345		S0003: 1 and S0214: 1.		
HOSGH28	686649	323	3 - 374	1346	Asn-101 to Lys-108.	S0214: 2, L0758: 2, L0596: 2, L0760: 1, L0055: 1, L0803: 1, L0526: 1 and L0779: 1.		
HOSGJ17	508870	324	108 - 284	1347	Ile-12 to Gln-19.	S0003: 2 and S0214: 1.		
HOSMD84	959483	325	529 - 762	1348		S0003: 2, L0748: 1, L0756: 1 and S0196: 1.		
HOSNO86	858938	326	150 - 341	1349	Gln-43 to Glu-54.	S0003: 2 and L0752: 1.		
HOSOE05	930946	327	13 - 192	1350	Gly-32 to Ala-38.	S0214: 2 and S0003: 1.		
HRDAB18	509019	328	85 - 276	1351	Arg-1 to Ser-18.	H0124: 2		
HRDAB60	509428	329	134 - 337	1352	Gln-40 to Asn-47, Val-49 to Lys-56.	H0124: 2 and L0530: 2.		
HRDAF07	954331	330	36 - 329	1353	Ser-47 to Gly-63.	H0124: 2		
HRDAF69	956269	331	1 - 225	1354		H0124: 2		
HRDAF90	531026	332	90 - 233	1355	His-31 to Thr-40.	H0124: 2		
HRDAH91	525525	333	79 - 240	1356	Gln-1 to Asn-20.	H0124: 2		
HRDBA76	534304	334	153 - 293	1357		H0124: 5		
HRDBC02	921144	335	117 - 284	1358		H0124: 2		

HRDBC30	530858	336	3 - 152	1359	Pro-28 to Arg-33.	H0124: 2	
HRDBC52	867169	337	72 - 278	1360	Asn-32 to Asn-43, Pro-56 to Cys-63.	H0124: 2	
HRDBD35	525526	338	1 - 189	1361		H0124: 2	
HRDBE07	954289	339	214 - 369	1362		H0124: 2	
HRDBE18	956267	340	145 - 264	1363	Ser-31 to Asn-40.	H0124: 2, L0776: 1, L0748: 1 and L0777: 1.	
HRDBE19	534495	341	161 - 394	1364	Thr-3 to Asp-10, Ser-21 to Asp-26.	H0124: 4	
HRDBE41	530856	342	3 - 158	1365	Glu-1 to Pro-10, Thr-14 to Trp-21, Gln-33 to Gln-42.	H0124: 2	
HRDBG59	507381	343	58 - 234	1366		H0124: 2	
HRDBI81	932761	344	116 - 316	1367		H0124: 2	
HRDBJ28	925457	345	234 - 350	1368		H0124: 2	
HRDBK03	925460	346	226 - 351	1369		H0124: 2	
HRDBL61	575229	347	152 - 334	1370	Gly-1 to Ser-12.	H0124: 2	
HRDBL75	524423	348	3 - 161	1371		H0124: 2	
HRDBM42	530849	349	1 - 375	1372	Asn-1 to Arg-9, Tyr-21 to Cys-27.	H0124: 2	
HRDBQ18	954274	350	1 - 183	1373	Asn-1 to Tyr-15.	H0124: 10	
HRDBQ38	533939	351	1 - 165	1374		H0124: 4, L0521: 1 and L0766: 1.	
HRDBQ64	879705	352	1 - 216	1375	Phe-1 to Gly-6, Ser-17 to Ser-23.	H0124: 34	
HRDBQ82	533947	353	244 - 393	1376	Ser-14 to Cys-24.	H0124: 10	
HRDBR04	927900	354	220 - 354	1377		H0124: 4	
HRDBR35	867167	355	29 - 175	1378	Ile-6 to Thr-21,	H0124: 5	

HRDBT72	507847	356	226 - 354	1379	Glu-35 to Ile-40.	AR089: 49, AR061: 16 H0124: 3		
HRDBU70	971700	357	2 - 88	1380	Ser-17 to Gly-24.	H0124: 3		
HRDCA61	921128	358	280 - 456	1381		H0124: 12		
HRDCB18	968554	359	2 - 232	1382	Pro-11 to Gln-17, Glu-51 to Ser-59.	H0124: 6		
HRDCD12	921796	360	247 - 432	1383		H0124: 12		
HRDDF49	867159	361	3 - 80	1384		H0124: 27		
HRDDF95	967837	362	244 - 435	1385		H0124: 15		
HRDDH84	867156	363	18 - 260	1386	Ser-7 to Ser-19, Arg-58 to Cys-70.	H0124: 2		
HRDDN54	932764	364	61 - 183	1387		H0124: 2		
HRDDN90	531117	365	118 - 324	1388		H0124: 2		
HRDDY26	526783	366	13 - 165	1389	Arg-13 to Ser-18.	H0124: 2		
HRDDY73	574336	367	96 - 374	1390		H0124: 2		
HRDDZ76	574324	368	3 - 92	1391	Leu-1 to Pro-10, Glu-12 to Ile-20.	H0124: 2		
HRDEB78	526861	369	12 - 152	1392		H0124: 3		
HRDEC91	747169	370	287 - 460	1393		H0124: 2		
	790096	1011	2 - 97	2034	Arg-11 to Glu-20.			
HRDED92	936045	371	15 - 218	1394	Cys-19 to Val-25.	H0124: 2		
HRDEG76	574326	372	168 - 254	1395	His-22 to Asn-29.	H0124: 2		
HRDEJ76	574335	373	17 - 109	1396	Glu-20 to Glu-27.	H0124: 2		
HRDEK44	574380	374	31 - 222	1397		H0124: 2		
HRDEL91	790374	375	2 - 217	1398	Thr-2 to Thr-8, Thr-23 to Ile-28.	H0124: 2		
HRDEO12	867140	376	3 - 194	1399	Asn-15 to Lys-21,	H0124: 2		

HRDEO76	952894	377	137 - 256	1400	Asp-49 to Ser-54. Pro-7 to Thr-12.	H0251: 1, H0124: 1 and S0242: 1.		
HRDEP31	766222	378	51 - 143	1401	Asp-1 to Leu-12, Leu-25 to Ser-31.	H0124: 2		
HRDEP75	574431	379	204 - 380	1402	Asp-5 to Lys-12.	H0124: 3		
HRDEQ30	506774	380	1 - 144	1403		H0124: 5 and L0749: 1.		
HRDEQ96	507543	381	189 - 428	1404		H0124: 4 and L0599: 1.		
HRDES52	867115	382	94 - 255	1405	Asn-1 to Glu-6, Ile-36 to Ala-42.	H0124: 2		
HRDES65	526823	383	212 - 385	1406	Pro-22 to Glu-27, Pro-49 to Thr-54.	H0124: 3		
HRDET67	825182	384	89 - 346	1407		H0124: 4		
HRDET91	827084	385	68 - 298	1408		H0124: 3		
HRDEU33	572905	386	78 - 320	1409	Pro-24 to Glu-32, Pro-49 to Arg-65.	H0124: 2		
HRDEU42	881296	387	56 - 325	1410	Arg-3 to Gly-9, Arg-53 to Thr-61.	H0124: 7		
HRDEU43	765813	388	40 - 159	1411		H0124: 3		
HRDEU61	575566	389	349 - 239	1412	Gly-1 to Tyr-7.	H0124: 7		
HRDEU78	573031	390	32 - 205	1413	Leu-8 to Gln-14, Glu-17 to Tyr-32.	H0124: 2		
HRDEU93	844316	391	3 - 461	1414	Arg-2 to Asp-10, Leu-28 to Phe-34, Asn-58 to Val-65, Pro-79 to Ser-84,	H0124: 3		

HRDEV13	574442	392	1 - 120	1415	Arg-106 to Pro-111.			
HRDEW02	848793	393	1 - 333	1416	Asp-18 to Thr-24.	H0124: 2		
HRDEW30	526812	394	83 - 238	1417	Ser-50 to Trp-56, Pro-95 to His-100.	H0124: 2		
HRDEW90	574288	395	110 - 271	1418		H0124: 4		
HRDEY14	574438	396	2 - 196	1419		H0124: 2		
HRDEZ06	936072	397	187 - 282	1420	Thr-32 to Ser-38, Ser-55 to Trp-64.	H0124: 3		
HRDEZ54	867127	398	2 - 307	1421		H0124: 2		
HRDEZ60	919386	399	2 - 220	1422	Gly-24 to Arg-29.	H0124: 2		
HRDEZ64	536668	400	2 - 79	1423	Trp-1 to Cys-7.	H0124: 2		
HRDEZ84	575553	401	230 - 382	1424	Asn-28 to Cys-33.	H0124: 7		
HRDFB47	508001	402	2 - 163	1425	Gln-1 to Trp-7, Ala-29 to Tyr-35.	H0124: 3		
HRDFB78	589478	403	37 - 381	1426	Ala-1 to Trp-9, Pro-11 to Ser-20.	H0124: 3		
HRDFC68	574205	404	2 - 172	1427		H0124: 4		
HRDFE73	574142	405	139 - 276	1428	Gly-10 to Phe-20.	H0124: 3		
HRDFE74	765750	406	152 - 268	1429		H0124: 3		
HRDFF42	953913	407	92 - 3	1430	Lys-1 to Pro-6, Ser-17 to Thr-26.	H0124: 2		
HRDFF62	574436	408	237 - 452	1431		H0124: 2 and L0748: 1.		
HRDFG25	574433	409	1 - 183	1432	Arg-2 to Asn-23.	H0124: 2		
HRDFG37	792517	410	3 - 197	1433	Gln-1 to Gln-7.	H0124: 2		
HRDFG46	574439	411	15 - 299	1434		H0124: 2		
HRDFH14	575578	412	24 - 140	1435	Lys-1 to Gln-17.	H0124: 4		

HRDFH24	575245	413	161 - 388	1436	Thr-1 to Arg-10, Ser-26 to Ile-31, Tyr-39 to Ile-46.	H0124: 2		
HRDFH25	953882	414	3 - 191	1437		H0124: 3		
HRDFH39	574558	415	62 - 268	1438	Thr-1 to Trp-11.	H0124: 2		
HRDFH77	953673	416	208 - 387	1439	Ser-17 to Gly-26, Glu-29 to Arg-37.	H0124: 5		
HRDFI13	574561	417	1 - 177	1440	Gly-1 to Ala-6.	H0124: 2		
HRDFJ71	574553	418	173 - 337	1441	Glu-10 to Ala-19.	H0124: 2		
HRDFK03	924925	419	3 - 305	1442	His-1 to Met-14.	H0124: 3		
HRDFK41	867106	420	185 - 328	1443		H0124: 2		
HRDFM18	574435	421	46 - 120	1444	Gly-7 to Glu-12.	H0124: 2		
HRDFN95	574565	422	130 - 38	1445	Arg-1 to Arg-7.	H0124: 2		
HRDFQ64	733847	423	56 - 268	1446	Val-1 to Gly-6, Gly-23 to His-32.	H0124: 2		
HRDFQ75	525524	424	3 - 149	1447	Glu-7 to Phe-15, Asn-32 to Lys-41.	H0124: 2		
HRDFT06	867109	425	57 - 245	1448	Pro-31 to Ser-36, Asn-47 to Glu-59.	H0124: 3		
HRDFT15	574549	426	3 - 134	1449		H0124: 4		
HRDFT45	506584	427	123 - 527	1450		AR061: 1, AR089: 0 H0124: 3		
HRDFT84	584823	428	3 - 458	1451	Pro-19 to Lys-25, Asp-30 to Pro-42, Pro-72 to Asp-83.	H0124: 3	6q16	136550, 602772
HRDFU48	573030	429	3 - 134	1452		H0124: 2		
HSHAX53	518795	430	1 - 213	1453		S0037: 3		
HSHBV66	523348	431	155 - 316	1454		S0037: 3		

HSBHV67	529483	432	188 - 301	1455			S0037: 2		
HSHCF34	529313	433	89 - 226	1456			S0037: 2		
HSKCS36	529163	434	2 - 187	1457			S0027: 2		
HSKCT33	866514	435	1 - 264	1458		Gly-1 to Gly-6, Arg-11 to Cys-22, Phe-65 to Lys-73.	S0027: 3		
HSKDA70	757183	436	98 - 613	1459			L0757: 4, L0806: 3, L0761: 2, L0800: 2, S0027: 2, L0770: 1, L0646: 1, L0764: 1, L0662: 1, L0653: 1, L0659: 1, L0787: 1, S0126: 1, S0390: 1, S0037: 1 and L0751: 1.		
HSKDJ16	661928	437	2 - 151	1460		Gly-1 to Arg-6.	S0027: 2		
HSKEF43	866410	438	1 - 270	1461		Pro-1 to Thr-11, Ser-23 to Thr-31, Pro-49 to Ile-57, Thr-75 to Ala-80.	S3014: 1 and S0027: 1.		
HSKEK63	744336	439	138 - 284	1462			H0135: 2 and S0027: 1.		
HSKEM02	969071	440	3 - 401	1463		Gln-31 to Gln-36, Thr-38 to Lys-44, Arg-58 to Arg-64, Tyr-72 to Val-78, Val-96 to Phe-101, Ala-105 to Gly-119.	S3014: 1 and S0027: 1.		
HSKET11	967000	441	2 - 427	1464		Gly-20 to Ser-27, Glu-88 to Lys-95.	S0027: 2		

HSKHJ11	965002	442	299 - 421	1465			S0027: 2 and S3014: 1.		
HSKHS71	911592	443	1 - 381	1466	Ala-94 to Cys-100.		AR089: 6, AR061: 4 S3014: 2		
HSKIT38	855173	444	199 - 381	1467			S3014: 1 and S0194: 1.		
HSKJS05	930979	445	1 - 57	1468			L0766: 1, S3014: 1 and S0206: 1.		
HSKKD70	916984	446	236 - 469	1469	Gly-43 to Trp-48, Met-50 to Asn-60.		S3014: 1 and S0028: 1.		
HSKKL06	934040	447	107 - 409	1470	Pro-13 to Ser-18, Gly-46 to Thr-52.		S0390: 1 and S3014: 1.		
HSKNO53	728210	448	384 - 533	1471			S3012: 1 and S0206: 1.		
HSKWA56	916496	449	272 - 436	1472			S0206: 2		
HSKWA78	731756	450	257 - 406	1473	Glu-10 to Asn-34.		S0206: 2		
HSKWA79	733394	451	148 - 312	1474	Ser-1 to Trp-16.		S0206: 2 and L0749: 1.		
HSKXG06	935455	452	221 - 90	1475			S0206: 2		
HSKXJ15	866373	453	121 - 450	1476			S3012: 1 and S0206: 1.		
HSKXN20	668928	454	116 - 223	1477	Pro-2 to Ile-16, Gln-18 to Lys-23.		S0206: 2		
HSKXP58	955073	455	3 - 134	1478	Pro-33 to Trp-38.		S0206: 2		
HSKXQ58	736045	456	24 - 170	1479			S0206: 2		
HSKYG66	698007	457	88 - 345	1480	Arg-7 to His-12, Pro-22 to Gln-28, Arg-70 to Pro-77.		S0206: 3 and L0758: 1.		
HSKYH52	466574	458	189 - 383	1481	Ser-21 to Lys-32.		S0206: 2		
HSKYJ96	921032	459	101 - 268	1482			H0251: 1 and S0206: 1.		
HSKZE12	970639	460	117 - 61	1483			S0027: 1 and S0206: 1.		
HSKZE32	959400	461	129 - 1	1484	Lys-2 to Cys-15.		S0027: 2, L0748: 2, L0751: 2 and S0192: 1.		

HSLAB77	772652	462	122 - 313	1485	Ala-21 to Gly-26.	S0028: 2		
HSLBO30	574086	463	1 - 210	1486	Ala-14 to Arg-21.	S0028: 2		
HSLBW19	671738	464	104 - 226	1487	Val-25 to Lys-32.	S0028: 2		
HSLBX08	959911	465	2 - 271	1488		S0028: 2		
HSLBX20	574004	466	139 - 435	1489	Leu-17 to Asp-22, Pro-30 to Glu-36, Asn-40 to Asn-46, Pro-61 to Ser-66, Arg-76 to Ile-88.	S0028: 2		
HSLBZ91	573987	467	3 - 284	1490	Val-17 to Glu-22.	AR089: 8, AR061: 5 S0028: 3		
HSLCB15	693455	468	170 - 631	1491	Thr-1 to Trp-7, Thr-9 to Gly-18, Gly-26 to Pro-40, Gln-53 to Asp-66, Ala-70 to Met-107, Glu-110 to Arg-136.	S0028: 2 and L0744: 1.		
HSLCJ46	529622	469	3 - 278	1492	Ser-87 to Asn-92.	S0028: 2		
HSLCJ47	908627	470	6 - 302	1493	Ser-8 to His-20, Glu-28 to Thr-34, Leu-64 to Gly-76.	S3014: 1 and S0028: 1.		
HSLCL38	951028	471	2 - 202	1494	Asp-24 to Cys-30.	S0028: 2		
HSLCP75	529631	472	75 - 353	1495	Pro-7 to Gln-14.	S0028: 2		
HSLCV95	793080	473	164 - 289	1496		S0028: 2		
HSLDA25	679301	474	1 - 297	1497	Ser-1 to His-9, Gln-32 to Asn-37, Tyr-58 to Leu-78.	S0028: 2		
HSLDB29	866340	475	7 - 402	1498		S0028: 2		

HSLDC06	936010	476	3 - 227	1499			S0028: 2		
HSLDG13	913664	477	17 - 232	1500	Arg-1 to Arg-18, Glu-28 to Asn-39.		S0028: 2		
HSLDI16	574014	478	104 - 184	1501	Ile-1 to Thr-6.		S0028: 2		
HSLDJ24	574050	479	1 - 264	1502	Gln-37 to Ile-43, Pro-50 to Leu-58, Glu-64 to Leu-69.		S0028: 2		
HSLDJ94	753657	480	40 - 243	1503	Val-17 to Pro-22, Thr-39 to Trp-45, Gln-63 to Cys-68.		H0251: 1 and S0028: 1.		
HSLDK43	675440	481	132 - 353	1504			S0390: 2 and S0028: 1.		
HSLDM32	699486	482	2 - 163	1505	Pro-8 to Arg-18, Phe-28 to Arg-35.		S0028: 2		
HSLDM79	526740	483	130 - 348	1506			S0028: 3		
HSLDP16	573210	484	2 - 277	1507			AR061: 0, AR089: 0 S0028: 2		
HSLDW65	689722	485	238 - 429	1508			S0028: 2		
HSLEB25	669654	486	125 - 343	1509	Gly-13 to Glu-24.		S0028: 2		
HSLEC25	572859	487	2 - 298	1510	His-35 to Ser-42, Asp-57 to Pro-62, Gly-70 to Gly-77.		S0028: 2		
HSLEC36	936003	488	1 - 282	1511	Ser-7 to Ala-13, Pro-54 to Cys-59.		S0028: 2		
HSLED38	709381	489	102 - 491	1512			AR061: 3, AR089: 2 S0126: 2 and S0028: 1.		
HSLED42	572860	490	38 - 388	1513	Arg-1 to Pro-8.		S0028: 2		
HSLEE46	572878	491	1 - 297	1514	Asp-1 to Asp-6.		S0028: 2		
HSLEF89	572883	492	45 - 257	1515			S0028: 3		

HSLEG74	825500	493	3 - 221	1516	Ser-12 to Trp-29.	S0037: 1 and S0028: 1.		
HSLEH57	584090	494	2 - 142	1517	Pro-1 to Trp-10, Ala-13 to Glu-18, Thr-31 to Trp-38, Glu-40 to Cys-47.	S0028: 2		
HSLEJ22	572863	495	59 - 247	1518	Gly-1 to Gly-10, Arg-35 to Gly-44.	S0028: 2		
HSLEI46	573212	496	1 - 288	1519		S0028: 2		
HSLEO70	841952	497	22 - 207	1520	Asn-20 to Glu-28, Gly-55 to Lys-62.	S0028: 2		
HSLEF34	706986	498	3 - 263	1521	Ala-8 to Gly-16, Ser-23 to His-49, Phe-73 to Ser-79.	S0028: 2		
HSLEFF91	572885	499	10 - 339	1522	Pro-63 to Lys-71.	S0028: 3, L0800: 1, L0803: 1, L0777: 1 and L0731: 1.		
HSLEFM86	785489	500	2 - 304	1523	Arg-13 to Gly-22.	S0028: 2		
HSLEFS42	948740	501	25 - 300	1524	Pro-1 to His-7, His-12 to Arg-24, Thr-32 to Gln-45, Arg-80 to Leu-85.	S0028: 2		
HSLEFS45	717782	502	2 - 136	1525	Arg-1 to Ile-8.	S0028: 2		
HSLEFT76	725788	503	106 - 396	1526		S0028: 2		
HSLEFT89	786061	504	73 - 390	1527		S0028: 2		
HSLEFU01	916448	505	83 - 412	1528		S0028: 2		
HSLEGD23	675872	506	35 - 448	1529	Phe-1 to Gly-6, Pro-46 to Gln-56.	S0028: 2		
HSLEGH26	681705	507	160 - 312	1530	Ile-17 to Gln-23,	S0028: 2		

HSLGK79	774049	508	3 - 389	1531	Arg-44 to Tyr-51. Pro-13 to Gly-22, Asp-57 to Ala-63, Ser-78 to Ala-88.	S0028: 2		
HSLGV91	780005	509	50 - 289	1532	Tyr-1 to His-6.	S0028: 2		
HSLGX20	669648	510	115 - 255	1533	His-8 to Ile-15, Tyr-32 to Thr-37.	S0028: 2		
HSLHA55	866273	511	99 - 404	1534		S0028: 3		
HSLHC22	673918	512	312 - 452	1535		S0028: 2 and L0754: 1.		
HSLHP20	669210	513	52 - 432	1536	Gly-29 to Phe-34.	S0028: 2		
HSLIA21	668116	514	3 - 125	1537	Pro-20 to Tyr-28, Pro-30 to Lys-35.	S0028: 2		
HSLIG54	713982	515	67 - 396	1538	Arg-1 to Gly-18, Ser-31 to Ser-37, Arg-39 to Gly-44.	S0028: 2		
HSLII61	918071	516	295 - 426	1539	His-35 to Ser-44.	S0250: 1, S0028: 1, L0748: 1 and L0750: 1.		
HSLIJ57	659533	517	3 - 389	1540	Arg-39 to Gln-44.	AR089: 1, AR061: 0 S0028: 2		
HSLJB11	966227	518	1 - 144	1541	Ala-1 to Trp-6.	S0390: 1 and S0028: 1.		
HSLJ21	670330	519	14 - 343	1542	Ser-1 to Asp-12, Ala-22 to Asn-28.	S0390: 1 and S0028: 1.		
HSLJJ83	727874	520	47 - 307	1543	Gly-19 to Asn-35.	S0390: 1 and S0028: 1.		
HSLJK88	923108	521	79 - 216	1544		S0390: 2		
HSLJN31	750394	522	3 - 251	1545		S0390: 1 and S0028: 1.		
HSLJN49	920062	523	83 - 394	1546	Pro-35 to Ser-41.	S0390: 2 and S0028: 1.		
HSLJN61	966267	524	160 - 498	1547	Glu-1 to Phe-6, Lys-12 to Pro-31,	S0390: 2 and S0028: 1.		

							Arg-41 to Ile-47, Glu-50 to Arg-55.				
HSLJN71	759941	525	16 - 213	1548			Pro-16 to Arg-22, Lys-29 to His-35.		S0390: 1 and S0028: 1.		
HSLJQ31	961447	526	151 - 399	1549					S0390: 2		
HSLJW53	866261	527	2 - 94	1550					S0390: 2		
HSLKC70	866256	528	102 - 422	1551					S0390: 1 and S0028: 1.		
HSRAX95	747078	529	61 - 324	1552			His-14 to Leu-21, Glu-34 to Leu-46, Glu-62 to Asn-67.		S0011: 2		
HSRBE02	921205	530	60 - 269	1553			Gln-19 to Arg-26, Gln-41 to Leu-47, Arg-53 to Phe-69.		S0011: 2		
HSRDE58	519542	531	32 - 181	1554			Glu-10 to Cys-15, Ser-21 to Cys-39.		S0022: 2		
HSRDI39	921749	532	144 - 386	1555			Ser-40 to Lys-47.		S0022: 4 and S0011: 1.		
HSRDJ68	530333	533	111 - 227	1556					S0022: 1 and S0011: 1.		
HSRDK92	838033	534	1 - 222	1557					S0022: 1 and S0011: 1.		
HSRDL32	530294	535	110 - 232	1558			Pro-1 to His-7, Glu-17 to Lys-30.		S0022: 2		
HSRDM42	523843	536	1 - 150	1559					S0022: 2 and S0011: 1.		
HSRDN23	530334	537	90 - 212	1560			Arg-16 to Glu-21, Leu-23 to Gly-32.		S0022: 2		
HSRDQ89	780221	538	6 - 137	1561					S0022: 1 and S0011: 1.		
HSRDS77	530289	539	148 - 243	1562					S0022: 1 and S0011: 1.		
HSREB43	524678	540	3 - 125	1563			Pro-7 to Cys-27, Tyr-32 to Lys-41.		S0011: 2		
HSREC27	753810	541	62 - 310	1564			Pro-15 to Ile-23,		S0011: 2		

						Ser-31 to Tyr-36, Ala-43 to His-48, Pro-54 to Arg-60.					
HSRED45	530233	542	3 - 146	1565				S0011: 2			
HSREG25	523815	543	156 - 323	1566		Val-22 to Phe-36.		S0011: 2 and S0022: 1.			
HSREG40	712779	544	1 - 513	1567		Val-22 to Pro-31, Pro-43 to Ser-51, Ala-55 to Ala-86, Ala-102 to Ile-120, Pro-122 to Val-148.		S0011: 1, S0242: 1 and S0194: 1.	17q21.3- q22	109270, 109270, 109270, 109270, 109270, 120150, 120150, 120150, 139250, 148065, 148080, 150200, 154275, 156490, 171190, 176960, 185800, 221820, 249000, 253250, 600119, 600119, 600525, 600852, 601844	
HSREG49	723267	545	1 - 165	1568				S0338: 1 and S0011: 1.			
HSRFC96	558385	546	62 - 178	1569		Met-11 to Asp-16, Ser-23 to Lys-29.		S0022: 2			
HSRFD34	575288	547	29 - 151	1570				S0022: 2			
HSRFD47	973782	548	163 - 357	1571				S0022: 6			
HSRFE58	556519	549	10 - 156	1572				S0022: 2			
HSRFF03	925369	550	33 - 143	1573				S0022: 2			
HSRFG30	920265	551	1 - 273	1574				S0022: 2			
HSRFR21	529767	552	109 - 243	1575		Ser-7 to Ser-12, Gln-21 to Trp-27.		S0022: 2			

HSRFZ71	557976	553	62 - 289	1576			S0022: 2		
HSRGA32	529726	554	134 - 268	1577			S0022: 2		
HSRGB23	974538	555	296 - 400	1578		Gly-2 to Gly-14.	S0022: 4		
HSRGE47	974539	556	2 - 214	1579		Lys-24 to Gln-34, His-41 to Arg-46.	S0022: 3		
HSRGG66	556518	557	2 - 112	1580			S0022: 2		
HSRGK48	535012	558	2 - 124	1581			S0022: 3		
HSRGQ30	534479	559	3 - 248	1582			S0022: 4, L0662: 1 and S0011: 1.		
HSRGS08	960211	560	7 - 195	1583			S0022: 3		
HSRGV79	921005	561	124 - 315	1584		Arg-53 to Thr-58.	S0022: 9		
HSRGW30	529624	562	170 - 310	1585			S0022: 2		
HSRGZ32	699561	563	1 - 240	1586			S0022: 5		
HSRHA45	974551	564	19 - 168	1587			S0022: 7		
HSSAE47	720685	565	193 - 318	1588		Ile-1 to Pro-10.	H0135: 2		
HSSAF46	508117	566	121 - 330	1589			H0135: 2		
HSSAN96	936108	567	57 - 251	1590			H0135: 2		
HSSAP44	508831	568	46 - 234	1591		Gln-7 to Arg-18.	H0135: 2		
HSSAV18	508832	569	90 - 200	1592		Ala-1 to Leu-7, Arg-27 to Gly-33.	H0135: 2		
HSSAV88	508829	570	62 - 241	1593		Asn-1 to Ser-17.	H0135: 2		
HSSBO48	871217	571	2 - 370	1594			H0135: 2		
HSSBO59	707683	572	259 - 402	1595		Ile-4 to Glu-18.	H0135: 2		
HSSCC04	928001	573	46 - 132	1596		Gly-1 to Asn-9.	H0135: 2		
HSSDJ02	871226	574	2 - 229	1597			H0135: 2		
HSSDL20	667599	575	2 - 172	1598		Ala-1 to Pro-8, Thr-19 to Pro-27.	H0124: 2 and H0135: 1.		
HSSDL94	526758	576	16 - 297	1599		His-10 to Arg-25.	H0135: 2		

HSSDR63	537329	577	1 - 225	1600	Ala-28 to Glu-34.	H0135: 2		
HSSDX20	783128	578	17 - 127	1601		H0135: 3		
HSSED56	625572	579	182 - 370	1602	Cys-30 to Arg-35.	H0135: 1 and S0027: 1.		
HSSEF29	689837	580	152 - 403	1603	Pro-41 to Met-46.	H0135: 2		
HSSEK75	766507	581	57 - 176	1604	Arg-10 to Cys-16.	H0135: 2		
HSSEU91	766573	582	86 - 175	1605	Ser-1 to Lys-8.	H0135: 1 and S0028: 1.		
HSSEU93	911261	583	116 - 370	1606	Asn-1 to Gly-17, Gln-23 to His-55, Glu-68 to Cys-77.	H0135: 2		
HSSEV89	572851	584	62 - 310	1607	Pro-21 to Asp-27, Val-50 to Cys-62.	H0135: 2	16	
HSSFF80	753589	585	3 - 299	1608	Gly-8 to Gly-14.	H0135: 2		
HSSFQ43	715318	586	209 - 328	1609	Asp-12 to Asn-21.	H0135: 2		
HSSFR41	707006	587	75 - 359	1610	Pro-13 to Pro-18, Ala-41 to Cys-50.	H0135: 2		
HSSFX54	708845	588	3 - 248	1611	Pro-42 to Trp-47, Trp-62 to Pro-68.	H0135: 2 and L0581: 1.		
HSSGC65	955064	589	2 - 403	1612	Ala-18 to Ala-24, Pro-26 to Asp-37.	H0135: 3 and L0761: 1.		
HSSGC66	319740	590	101 - 3	1613		H0135: 2		
HSSGC72	760648	591	2 - 91	1614		H0135: 2		
HSSGD37	739505	592	2 - 160	1615	Ser-47 to Ser-52.	H0135: 2		
HSSGH47	720367	593	66 - 353	1616	Gln-1 to Lys-8.	H0135: 2		
HSSGI20	668919	594	114 - 341	1617	Tyr-26 to Glu-31.	H0135: 2		
HSSGI75	767325	595	255 - 16	1618		H0135: 2		
HSSGI91	789411	596	3 - 305	1619	Tyr-18 to Pro-27, Gln-32 to Leu-41, Pro-90 to Gly-99.	H0135: 2		

HSSGK96	960636	597	72 - 287	1620	Gly-12 to His-19.	H0135: 2		
HSSGL55	766115	598	177 - 545	1621		H0135: 4 and L0747: 1.	7q32	180105, 190900, 222800, 246900
HSSGL78	788924	599	211 - 390	1622		H0135: 2		
HSSGM62	707685	600	2 - 409	1623	Ser-1 to Tyr-6, Met-87 to Tyr-93, Ala-108 to Ala-113.	H0135: 2		
HSSGN47	707003	601	3 - 338	1624	His-1 to Gly-28, Ser-54 to Gly-79, Pro-81 to Lys-102.	H0135: 2, L0794: 2, L0636: 1 and L0749: 1.	19q13.1	164731, 172400, 172400, 180901, 180901, 221770, 248600, 600918, 602716
HSSHA92	792714	602	169 - 309	1625	Leu-26 to Asn-38.	H0135: 2		
HSSJN44	716573	603	340 - 438	1626		H0124: 1 and H0135: 1.		
HSSJN49	708841	604	93 - 305	1627	Trp-1 to Asn-6, Gln-37 to Cys-52, Pro-64 to Lys-70.	H0135: 2		
HSSJU66	653212	605	1 - 204	1628	Gly-1 to Ser-6.	H0135: 2		
HSSJV60	970749	606	155 - 373	1629	Arg-1 to Ser-7.	H0135: 2 and L0779: 1.		
HSSKB40	711130	607	68 - 325	1630	Gly-1 to Pro-12, Phe-25 to Asn-34, Arg-40 to Ala-46, Pro-73 to Trp-78, Gln-80 to Pro-86.	H0135: 1, S0037: 1 and L0754: 1.	22	
HSSMT78	712468	608	123 - 380	1631	Gly-6 to Arg-12.	H0135: 2		
HYBAE74	925074	609	36 - 239	1632		H0041: 2		

HYBAG11	967880	610	1 - 207	1633			H0041: 2		
HYBAU83	732419	611	106 - 234	1634			H0041: 2		
HYBAX25	456251	612	97 - 354	1635	Leu-29 to Lys-34, Gly-63 to Cys-69.		H0041: 2		
HYBAY40	531202	613	2 - 298	1636			H0041: 2		
HYBBB24	584989	614	19 - 150	1637			H0041: 2, L0764: 1, L0766: 1 and L0759: 1.		
HYBBI18	584991	615	174 - 350	1638	Lys-27 to His-39.		H0041: 2		
HYBBJ30	693345	616	3 - 215	1639			H0041: 1 and S0011: 1.		
HYBBL17	691328	617	2 - 166	1640	Arg-20 to Ala-27.		H0041: 2		
HYBBK83	505138	618	489 - 127	1641			H0041: 1		
	510490	1012	164 - 544	2035	Ala-40 to Gln-45, Gln-55 to Thr-65, Pro-93 to Ser-101.				
HYBBG93	531201	619	2 - 70	1642			H0041: 1		
HYBAY92	792923	620	193 - 438	1643			L0748: 2 and H0041: 1.		
HYBAW03	925068	621	110 - 295	1644			H0041: 1 and L0758: 1.		
HYBAH65	518736	622	337 - 606	1645	Lys-1 to Gly-7, Arg-12 to Pro-18, Val-22 to Trp-29, Pro-41 to Leu-49, Glu-51 to Asp-64.		L0748: 7, H0041: 1 and L0747: 1.		
HYBAG53	669602	623	296 - 475	1646			L0748: 2, H0041: 1 and L0744: 1.		
HYBAF63	745585	624	308 - 508	1647			H0041: 1 and L0756: 1.		

HSSMZ93	530752	625	7 - 246	1648	Arg-1 to Asn-12, Gln-31 to Gly-37, Pro-48 to Gly-55.	H0135: 1		
HSSMZ01	921800	626	72 - 278	1649	Thr-18 to Val-23, Leu-39 to Gln-45.	H0135: 1		
HSSMW90	975081	627	3 - 191	1650		H0135: 1 and L0755: 1.		
HSSMT76	928421	628	2 - 193	1651	Trp-36 to Pro-45.	H0135: 1		
HSSMT70	530758	629	59 - 214	1652	Pro-22 to Ile-28.	H0135: 1		
HSSMP20	854092	630	144 - 299	1653	Asp-2 to Ala-12, Leu-21 to Ser-45.	H0135: 1 and L0754: 1.		
HSSKD17	726525	631	92 - 511	1654	Gln-1 to Gly-10, Arg-15 to Arg-22, Leu-49 to Asp-58, Arg-72 to Trp-78.	H0135: 1 and L0747: 1.		
HSSJQ60	975185	632	1 - 147	1655	Lys-30 to Phe-37.	H0135: 1		
HSSJP81	911334	633	153 - 440	1656	Arg-11 to Leu-26, Pro-29 to Gly-38, Leu-78 to Ser-84.	H0135: 1, L0766: 1 and L0438: 1.		
HSSJL22	871170	634	141 - 569	1657	Ser-37 to Lys-49.	H0135: 1		
	894004	1013	528 - 358	2036	Val-34 to Pro-39.			
HSSJK65	747891	635	37 - 288	1658		L0748: 2, H0135: 1 and L0749: 1.		
HSSJH78	773558	636	84 - 218	1659	Ile-13 to Cys-19, Ser-23 to Glu-28.	H0135: 1, L0439: 1 and L0747: 1.		
HSSJA08	959336	637	387 - 536	1660		L0764: 2, H0135: 1 and L0804: 1.		
HSSGK12	970714	638	236 - 370	1661	Phe-10 to Lys-17.	AR051: 144, AR050:		

								132, AR054: 132 H0135: 1			
HSSGI84	781975	639	335 - 505	1662		Lys-9 to Lys-14, Ser-33 to Arg-40.		H0135: 1 and L0748: 1.			
HSSGD96	796410	640	1 - 111	1663		Gly-1 to Ser-16.		H0135: 1			
HSSGD82	779899	641	168 - 524	1664		Met-55 to Gly-66.		H0135: 1 and L0741: 1.			
HSSGD56	608144	642	209 - 379	1665		Arg-1 to Asp-10, Gln-16 to Lys-21.		H0135: 1			
	975065	1014	34 - 204	2037		Arg-1 to Asp-10, Gln-16 to Lys-21.					
HSSFW84	781973	643	36 - 371	1666		Gly-19 to Gly-28, Gly-43 to Gln-67, Ser-86 to Glu-93, Leu-95 to Val-101.		H0135: 1 and L0439: 1.			
HSSFU84	888462	644	1 - 402	1667		Pro-6 to Thr-15, Ala-20 to Arg-36, Pro-38 to Gln-85.		AR051: 21, AR054: 16, AR050: 10 H0135: 1			
	959735	645	243 - 500	1668				H0135: 1 and L0365: 1.	Xq28	300031, 300044, 300048, 300049, 300049, 300055, 300100, 300100, 300104, 300126, 301201, 301590, 302060, 302060, 302060, 302060, 302960, 303700, 303800, 303900,	

									304800, 305900, 305900, 305900, 306700, 306995, 308310, 308840, 308840, 308840, 309200, 309548, 309620, 309900, 310300, 310400, 310460, 310460, 311300, 311510, 314300, 314400
HSSFK90	788687	646	423 - 151	1669				H0135: 1	
HSSFB73	955200	647	334 - 137	1670				H0135: 1 and L0748: 1.	
HSSEU40	891055	648	101 - 238	1671	His-6 to Ala-17, Thr-37 to Trp-44.	AR054: 8, AR051: 3, AR050: 1 H0135: 1 and L0749: 1.			
HSSEP69	871211	649	30 - 287	1672				H0135: 1	
HSSEI90	789157	650	2 - 370	1673	Phe-7 to Arg-13.			H0135: 1 and L0748: 1.	
HSSEG25	679351	651	150 - 338	1674	Pro-10 to Asp-15, Leu-38 to Gly-54.	L0766: 2, L0747: 2, H0135: 1, L0796: 1, L0789: 1 and L0752: 1.			
HSSEF33	702701	652	274 - 522	1675				H0135: 1 and L0748: 1.	
HSSEC79	775312	653	1 - 267	1676	Thr-24 to Asp-43, Pro-53 to Asp-58,	H0135: 1 and L0592: 1.			

HSSDQ07	880720	654	81 - 419			Cys-62 to Gly-67.			
HSSDI03	924975	655	107 - 283	1677	1678	Gly-6 to Thr-12. Val-1 to Cys-13.	H0135: 1 H0135: 1, L0538: 1 and L0747: 1.		
HSSDH37	575460	656	18 - 251	1679	1680	Pro-2 to Ser-11. Arg-1 to Ser-7, Gln-20 to Gly-28.	H0135: 1 H0135: 1 and L0439: 1.		
HSSDC50	724696	657	1 - 219	1681	1682		H0135: 1 L0766: 2 and H0135: 1.		
HSSCC14	600216	658	647 - 399	1683			H0135: 1 and L0439: 1.		
HSSAZ04	933015	659	15 - 170	1684	1685		H0135: 1 H0135: 1 and L0747: 1.		
HSSAY34	703345	660	104 - 412	1686			H0135: 1 and L0606: 1.		
HSSAP68	564334	661	704 - 417	1687	1688	Ser-13 to Ser-19, Asp-42 to Arg-49, Ser-95 to Lys-104, Gln-145 to Thr-150.	AR050: 62, AR054: 51, AR051: 51 H0135: 1		
HSSAJ89	875882	662	89 - 316	1689			L0666: 1 and S0011: 1.		
HSSAE52	871244	663	10 - 180	1690	1691	Thr-5 to Asn-13, Pro-40 to His-46, Phe-54 to Phe-59. Lys-1 to Gln-8.	L0748: 1 and S0011: 1.		
HSSAA15	965347	664	42 - 491	1692			S0011: 1 S0011: 1		
HSRAY10	961237	665	28 - 240	1693					
HSRAS82	780222	666	46 - 237	1694					
HSRAF70	524680	667	194 - 379	1695					
HSRAF11	967886	668	176 - 271	1696					

HSRAD72	539530	669	3 - 221	1692		S0011: 1			
HSRAD65	871268	670	1 - 135	1693	Asn-1 to Arg-12.	S0011: 1	8p21-p12	152760, 173370, 180100, 185430, 270800, 277700, 602629	
HSRAD53	525490	671	60 - 335	1694	Ala-1 to Cys-14, Val-72 to Trp-77.	S0011: 1			
HSRAD49	722134	672	211 - 390	1695		L0761: 1, L0749: 1, L0758: 1 and S0011: 1.			
HSRAD31	524845	673	136 - 249	1696	Cys-2 to Pro-11.	S0011: 1			
HSRAD10	968614	674	236 - 445	1697	Lys-10 to Gly-19, Ala-23 to Cys-29.	L0803: 1 and S0011: 1.			
HSRAD03	925505	675	120 - 305	1698	Pro-10 to Met-18, Pro-48 to Glu-62.	S0011: 1			
HSRAB87	823174	676	3 - 122	1699	Thr-10 to Gly-18.	S0011: 1			
HSRAB82	522945	677	49 - 246	1700	Leu-44 to Arg-50.	S0011: 1			
HSRAB76	508105	678	48 - 299	1701		S0011: 1			
HSRAB36	522946	679	2 - 163	1702		S0011: 1			
HSRAB34	706996	680	3 - 146	1703	Phe-1 to Asn-12.	S0011: 1			
HSRAB08	960411	681	2 - 145	1704	Ile-1 to Lys-6.	S0011: 1			
HSRAA86	527194	682	74 - 202	1705		S0011: 1			
HSRAA80	937640	683	2 - 325	1706	Ile-1 to Cys-10, Arg-95 to Phe-106.	AR061: 150, AR089: 93 S0011: 1			
HSRAA64	955314	684	220 - 327	1707		S0011: 1			
HSRAA51	522834	685	3 - 326	1708	Ser-16 to Gly-27, Asp-48 to Ala-53, Thr-70 to Ser-77.	S0011: 1			

HSRAA39	719712	686	1 - 174	1709	Pro-17 to Trp-22.	S0011: 1		
HSRAA37	522837	687	29 - 127	1710	Thr-7 to His-13.	S0011: 1		
HSRAA24	795855	688	3 - 446	1711	Phe-1 to Leu-8, Pro-72 to Trp-86.	S0011: 1		
HSRAA23	524795	689	3 - 251	1712	Pro-8 to His-27, Thr-56 to Ser-61, Leu-77 to Phe-83.	S0011: 1		
HSLKB62	905738	690	212 - 937	1713	Glu-84 to Trp-92, Asn-106 to Gly-115, Lys-184 to Arg-191.	AR050: 220, AR051: 151, AR054: 146, AR061: 7, AR089: 2 S0390: 1		
HSLKB37	929743	691	171 - 374	1714		L0776: 2, L0748: 2, L0598: 1, L0529: 1, S0390: 1 and L0758: 1.		
HSLKA06	934638	692	1 - 222	1715	Gln-8 to Arg-14, Met-21 to Thr-27.	L0659: 1, L0809: 1 and S0390: 1.		
HSLJJ62	742895	693	173 - 436	1716	His-22 to Tyr-32.	L0748: 3 and S0390: 1.		
HSLJF33	938811	694	3 - 521	1717	Glu-70 to Gly-76.	AR089: 1, AR061: 1 S0390: 1		
HSLJD02	965826	695	47 - 907	1718	Leu-53 to Gln-58, Phe-162 to Gly-167, Gln-282 to Ala-287.	AR054: 7, AR051: 1, AR089: 1, AR061: 1, AR050: 0 S0390: 1		
HSLJJ48	721248	696	64 - 570	1719		S0028: 1 and L0748: 1.		
HSLIG07	952493	697	269 - 454	1720	Ser-19 to Asp-24.	L0766: 2, L0740: 2, L0803: 1, S0028: 1, L0745: 1 and L0759: 1.		
HSLJH03	923393	698	163 - 321	1721	Asn-27 to His-34.	S0028: 1 and L0592: 1.		

HSLIC21	670359	699	189 - 512	1722	Pro-3 to Ser-10.	L0742: 2, S0028: 1 and L0366: 1.		
HSLHZ82	779067	700	320 - 526	1723		S0028: 1 and L0748: 1.		
HSLHZ10	963808	701	59 - 307	1724	Val-24 to Asn-29, Arg-56 to Gly-64.	S0028: 1 and L0361: 1.		
HSLHV27	964075	702	983 - 21	1725	His-8 to Gly-18.	AR050: 5, AR061: 2, AR054: 1, AR089: 1 S0028: 1		
HSLHG49	722570	703	162 - 290	1726		L0438: 1, S0028: 1 and L0439: 1.		
HSLHC40	710681	704	230 - 400	1727		L0755: 2 and S0028: 1.		
HSLGY08	959371	705	215 - 397	1728	Tyr-4 to Ser-12, His-23 to Leu-29.	S0028: 1 and L0742: 1.		
HSLGQ48	720956	706	141 - 413	1729	Glu-2 to Thr-9.	L0438: 1, S0028: 1 and L0439: 1.		
HSLGP07	953305	707	224 - 442	1730	Asp-7 to Arg-15.	S0028: 1 and L0753: 1.		
HSLGO19	668634	708	115 - 543	1731		L0665: 1, S0028: 1, L0748: 1 and L0750: 1.		
HSLGN78	773565	709	1 - 156	1732		S0028: 1 and L0591: 1.		
HSLGN52	466026	710	3 - 266	1733	Thr-26 to Gln-40, Glu-47 to Arg-53.	S0028: 1 and L0740: 1. 12		
HSLGK46	719031	711	2 - 226	1734	Gln-8 to Asn-15, His-23 to Gln-28.	S0028: 1 and L0601: 1.		
HSLGK26	929286	712	422 - 607	1735		S0028: 1 and L0748: 1. 1q12-1q21.2	104770, 107670, 110700, 145001, 146760, 146790, 159001, 191315, 600897, 601412,	

HSLGK23	675266	713	176 - 343	1736					601652, 601863, 602491
HSLGI37	708824	714	120 - 452	1737	Thr-80 to Cys-87.		L0747: 2, L0766: 1 and S0028: 1.		
HSLGI76	770035	715	379 - 558	1738			S0028: 1 and L0439: 1.		
HSLGI67	465989	716	47 - 253	1739			S0028: 1 and L0748: 1.		
HSLGH70	871888	717	57 - 227	1740	Pro-23 to Leu-30.		L0439: 6 and S0028: 1.		
HSLGG86	784703	718	38 - 202	1741			S0028: 1 and L0745: 1.		
HSLGG79	775146	719	1 - 126	1742	Asp-1 to Thr-16.		S0028: 1 and L0439: 1.		
HSLGA79	774051	720	2 - 151	1743			S0028: 1 and L0740: 1.		
HSLGA45	717776	721	210 - 13	1744	Pro-9 to His-17, Gly-19 to Gly-24, Gly-30 to Ile-38, Leu-42 to Lys-51, Pro-54 to Asn-66.		S0028: 1 and L0599: 1.		
HSLGA24	955333	722	805 - 284	1745	Pro-45 to Arg-50, Glu-56 to Ser-62, Ser-70 to Glu-76, Asp-141 to Arg-149.		S0028: 1 and L0777: 1.		
HSLFU18	666405	723	576 - 842	1746	Asp-7 to Lys-13, Asn-63 to Tyr-75.		AR089: 14, AR061: 3 S0028: 1		
							L0770: 3, L0777: 3, L0731: 3, L0780: 2, L0040: 1, L0764: 1, L0766: 1, L0804: 1, L0809: 1, L0790: 1, L0438: 1, S0028: 1, L0439: 1, L0751: 1, L0745: 1 and L0749: 1.		

HSLFT29	680451	724	1 - 462	1747	Glu-1 to Phe-8, Met-55 to Leu-64, Gly-93 to His-99, Ala-135 to Cys-141.	AR089: 2, AR061: 2 S0028: 1		
HSLFN96	796375	725	3 - 167	1748	Gln-23 to Arg-39.	S0028: 1		
HSLFT01	876881	726	115 - 342	1749	Asp-12 to Thr-18.	S0028: 1 and L0754: 1.		
HSLD70	757319	727	327 - 515	1750	Ser-40 to Ser-47, Pro-52 to Gly-60.	S0028: 1, L0777: 1 and L0759: 1.		
HSLB84	783130	728	122 - 280	1751		S0028: 1 and L0754: 1.		
HSLDW24	779689	729	33 - 209	1752	Tyr-38 to His-45.	L0756: 2 and S0028: 1.		
HSLDT25	949079	730	1544 - 867	1753		AR051: 22, AR050: 20, AR054: 19, AR089: 17, AR061: 9 S0028: 1		
HSLDR18	578926	731	148 - 270	1754	Glu-1 to Gly-10, Glu-21 to Asn-32.	S0028: 1		
HSLDR05	932128	732	83 - 232	1755	Arg-1 to Asp-7.	S0028: 1		
HSLDP66	866331	733	189 - 401	1756		S0028: 1		
HSLDO01	916969	734	33 - 113	1757		S0028: 1		
HSLDM82	780055	735	3 - 428	1758	Tyr-18 to Leu-23, Tyr-64 to Ser-70, Glu-77 to Arg-82.	L0361: 2 and S0028: 1. 1p36.3	120550, 120570, 120575, 153454, 236250, 256700	
HSLDF25	430328	736	363 - 1	1759	Gln-38 to Cys-43, Val-55 to Cys-62, Pro-64 to Pro-69, Lys-76 to Phe-83, Ser-85 to Arg-91, Lys-113 to Arg-121.	S0028: 1		

	677994	1015	251 - 123	2038	Pro-1 to Thr-13, Leu-31 to Leu-37.			
HSLCY75	766533	737	326 - 550	1760	Leu-22 to Arg-27.	S0028: 1 and L0749: 1.		
HSLCX61	742031	738	343 - 507	1761	Gly-4 to Tyr-18, Gly-48 to Gly-55.	AR089: 3, AR061: 1 L0439: 2 and S0028: 1.		
HSLCF96	637670	739	355 - 1248	1762	Val-2 to Trp-7, Lys-9 to Trp-18, Gln-20 to Gly-25, Gln-79 to His-85, Pro-134 to Asp-139, Asp-164 to Thr-171, Pro-223 to Arg-228.	AR054: 38, AR050: 26, AR051: 25, AR061: 2, AR089: 1 S0028: 1		
	954777	1016	1332 - 430	2039	Thr-1 to Cys-6, Ser-52 to Gly-57, Gln-111 to His-117.			
HSLBW39	705630	740	1 - 432	1763	Asp-2 to Trp-28, Pro-33 to Asn-39, Pro-88 to Gln-104.	S0028: 1 and L0591: 1.		
HSKZE91	790166	741	75 - 335	1764	Val-1 to Leu-7, Pro-11 to Glu-20.	S0027: 1 and L0605: 1.		
HSKYG48	721631	742	3 - 296	1765	Arg-6 to Lys-17.	S0206: 1		
HSKXA69	754258	743	2 - 169	1766		L0748: 2, S0206: 1 and L0599: 1.		
HSKKE11	965857	744	90 - 245	1767	Arg-1 to Gln-10, Thr-41 to Gln-48.	S3014: 1 and L0750: 1.		
HSKJR15	866396	745	59 - 406	1768	Gln-11 to Gly-18, Asn-25 to Ser-30.	AR089: 1, AR061: 0 L0666: 1, S3014: 1 and L0756: 1.		

HSK1C88	866402	746	154 - 357	1769	Arg-52 to Gln-58.	L0809: 1 and S3014: 1.		
HSK1I90	788894	747	482 - 613	1770		L0599: 2 and S3014: 1.		
HSKHZ47	720286	748	400 - 534	1771	Tyr-1 to Tyr-6.	L0745: 3 and S3014: 1.		
HSKHT93	957866	749	245 - 415	1772		L0766: 1 and S3014: 1. 5q11	253200, 600887	
HSKHP10	964568	750	136 - 240	1773		S3014: 1 and L0779: 1.		
HSKGS69	755046	751	3 - 335	1774	Asn-23 to Pro-31.	S3014: 1, L0748: 1 and L0749: 1.		
HSKEH21	941976	752	2 - 703	1775	Leu-26 to Gly-38, Leu-101 to Thr-116, Glu-144 to Val-151, Pro-177 to Pro-183, Thr-188 to Thr-195, Phe-203 to Asn-234.	AR061: 11, AR089: 4 S0027: 1		
HSKDC06	935452	753	174 - 332	1776		S0027: 1 and L0599: 1.		
HSKCR54	922730	754	86 - 547	1777	Gly-45 to Arg-50.	AR061: 8, AR089: 7 S0027: 1 and L0749: 1.		
HSKCD43	714389	755	3 - 188	1778		L0759: 2, S0027: 1 and 6q21 L0748: 1.	120110, 121014, 601666, 602772	
HSKBW86	785783	756	1 - 180	1779	Tyr-12 to Ile-24, Glu-43 to Lys-49.	AR089: 6, AR061: 3 S0027: 1		
HSKBW62	521937	757	23 - 175	1780		S0027: 1		
HSKBW21	671383	758	46 - 141	1781		S0027: 1 and L0779: 1.		
HSKBV67	561585	759	90 - 257	1782	Leu-15 to Ser-21.	S0027: 1		
HSKAE10	968508	760	640 - 464	1783	Thr-17 to Arg-22.	L0752: 2, L0803: 1 and S0027: 1.		
HSKAC29	535402	761	184 - 375	1784		S0027: 1		
HSJCA03	925252	762	213 - 362	1785		S0032: 1 and L0758: 1.		
HSJAY64	866540	763	123 - 284	1786	Pro-4 to Gln-11,	S0032: 1 and L0361: 1.		

HSJAB49	723261	764	209 - 337	1787	Cys-16 to Gly-21.	S0032: 1 and L0748: 1.		
HSHCL04	840406	765	640 - 1053	1788	Gly-1 to Ser-10.	AR051: 23, AR050: 17, AR054: 12, AR061: 5, AR089: 4 S0037: 1		
	957191	1017	331 - 2	2040	Arg-34 to Asn-39.			
	957192	1018	3 - 173	2041	Arg-22 to Asn-27.			
	957193	1019	344 - 192	2042				
HSHCK86	785392	766	1 - 291	1789		S0037: 1		
	792112	1020	574 - 353	2043	Gly-22 to Gln-34, Tyr-48 to Glu-56.			
HSHCI63	468536	767	73 - 336	1790	Val-19 to Tyr-25, Gln-82 to Ser-87.	S0037: 1		
	470736	1021	478 - 359	2044				
HSHBU07	866636	768	227 - 457	1791	Lys-3 to Lys-15.	S0037: 1		
HSHAH05	932689	769	209 - 96	1792	Gly-31 to Gln-37.	S0037: 1 and L0754: 1.		
HSCAF60	537444	770	59 - 199	1793	Arg-1 to Thr-8, Lys-16 to Asn-21.	S0118: 1		
	924698	771	187 - 357	1794	Lys-1 to Trp-18, Thr-36 to Ser-44.	H0124: 1 and L0748: 1.		
HRDFU03	590391	772	261 - 464	1795	His-1 to Asp-22, Pro-51 to Lys-58.	H0124: 1, L0387: 1, L0747: 1 and L0588: 1.		
HRDFG13	925350	773	1 - 249	1796		H0124: 1 and L0759: 1.		
HRDFF47	740594	774	1 - 114	1797		H0124: 1, L0598: 1, L0655: 1 and L0745: 1.		
HRDFD56	733556	775	47 - 178	1798		H0124: 1, L0439: 1,		

HRDFA03	867122	776	405 - 602	1799			L0745: 1 and L0756: 1.		
							AR054: 74, AR051: 68, AR050: 63 H0124: 1		
HRDEZ73	774414	777	21 - 254	1800		Gln-52 to Cys-57.	L0777: 2, H0124: 1, L0774: 1, L0743: 1, L0744: 1, L0757: 1 and L0758: 1.		
HRDEX24	867123	778	112 - 258	1801		Met-1 to Lys-6, Pro-13 to Asp-19.	L0731: 2, H0124: 1, L0800: 1, L0803: 1 and L0804: 1.		
HRDER90	789140	779	3 - 428	1802			L0748: 2, H0124: 1 and L0592: 1.		
HRDER35	707569	780	66 - 266	1803			H0124: 1 and L0748: 1.		
HRDEP20	690456	781	2 - 274	1804			H0124: 1, L0755: 1 and L0604: 1.		
HRDEK53	867137	782	2 - 181	1805			H0124: 1 and L0749: 1.		
HRDEI33	487523	783	123 - 31	1806			H0124: 1		
	867143	1022	260 - 556	2045					
	974260	1023	3 - 245	2046		Ala-3 to Ala-10, Ser-49 to Thr-74, Pro-76 to Lys-81.			
HRDDX67	460145	784	1 - 189	1807			H0124: 1		
	462510	1024	243 - 115	2047					
HRDDX01	921501	785	388 - 200	1808		Thr-27 to Trp-42.	H0124: 1, L0659: 1, L0783: 1 and L0779: 1.		

HRDDU41	712572	786	27 - 281	1809	Asn-46 to Ser-55.	H0124: 1		
HRDDR39	867151	787	1 - 222	1810		H0124: 1 and L0777: 1.		
HRDDQ55	490884	788	278 - 126	1811	His-3 to Asp-11, Leu-13 to Glu-26, Pro-46 to Gly-51.	H0124: 1		
	514848	1025	188 - 397	2048	Lys-8 to His-14.			
HRDCD44	715769	789	3 - 197	1812		H0124: 1 and L0740: 1.		
HRDBH52	728715	790	48 - 251	1813	Lys-4 to Lys-10, Pro-39 to Glu-46.	H0124: 1, L0748: 1 and L0747: 1.		
HRDAB42	800333	791	55 - 429	1814	Pro-11 to Arg-16, Pro-27 to Ser-32, Gln-53 to Thr-63.	H0124: 1 and L0748: 1.		
HOSOW01	914804	792	19 - 153	1815	Leu-10 to Pro-16, Leu-39 to Ser-45.	L0748: 2 and S0003: 1.		
HOSNO25	974291	793	417 - 566	1816		S0003: 1		
HOSMP95	948496	794	3 - 278	1817	Ser-2 to Leu-24, Pro-33 to Lys-45.	L0748: 5 and S0003: 1.		
HOSGN29	830653	795	1 - 432	1818	Ser-12 to Thr-27, Pro-32 to Glu-39, Gly-48 to Ile-55, Ile-59 to Leu-80, Gln-108 to Leu-113, Pro-121 to Tyr-131.	S0214: 1 and L0777: 1.		
HOSFV77	856933	796	468 - 659	1819	Leu-27 to Met-32.	S0214: 1, L0439: 1, L0749: 1 and L0595: 1.		
HOSFU59	739262	797	94 - 255	1820	Lys-1 to Leu-11.	S0214: 1 and L0731: 1.		

HOSFL57	734709	798	231 - 365	1821			S0214: 1 and L0754: 1.		
HOSFL07	953183	799	464 - 583	1822			L0766: 2, L0471: 1, S0214: 1, L0748: 1, L0749: 1 and L0756: 1.	1p35	118210, 120550, 120570, 120575, 121800, 130500, 133200, 138140, 138971, 171760, 171760, 172411, 185470, 230350, 255800, 602771
HOSFK40	711140	800	117 - 332	1823		Glu-5 to Ser-16, Gly-49 to Pro-57, Arg-62 to Met-72.	L0803: 2, S0214: 1, L0806: 1, L0788: 1, L0779: 1, L0596: 1 and L0599: 1.		
HOSFI46	719021	801	112 - 300	1824			S0214: 1 and L0756: 1.		
HOSFC66	750560	802	311 - 574	1825			S0214: 1 and L0602: 1.		
HOSFB04	615200	803	238 - 426	1826		Thr-20 to Phe-29, Tyr-40 to Gly-46.	L0439: 3 and S0214: 1.		
HOSDR12	971169	804	259 - 459	1827		Glu-22 to Glu-31.	S0003: 1		
HOSDQ78	858983	805	123 - 290	1828		Ser-1 to His-11, Val-22 to Trp-27.	S0003: 1		
HOSDP27	682113	806	157 - 456	1829		Pro-36 to Thr-43.	S0003: 1 and L0740: 1.		
HOSDG79	781787	807	3 - 590	1830		Leu-4 to Lys-17.	L0748: 2, S0003: 1 and L0749: 1.		
HOSDA04	951842	808	520 - 362	1831			S0003: 1 and L0731: 1.		
HOSCV06	960555	809	59 - 304	1832		Glu-5 to Gly-15, Pro-36 to Arg-42, Pro-58 to Asp-70.	AR089: 8, AR061: 7 S0003: 1, L0498: 1 and L0599: 1.		
HOSCT25	783692	810	155 - 325	1833		Ser-1 to Asn-9,	S0003: 1 and L0748: 1.		

HOSCP67	753874	811	158 - 370		Ala-16 to Lys-22. Lys-15 to Tyr-20, Ser-61 to Thr-71.	L0591: 2 and S0003: 1.		
HOSCO73	764756	812	2 - 163	1835		S0003: 1 and L0599: 1.		
HOSBY89	787182	813	254 - 364	1836	Thr-12 to Ser-26.	L0748: 2 and S0003: 1.		
HOSBX46	719414	814	270 - 365	1837	Phe-6 to Trp-11.	L0756: 2 and S0003: 1. 14		
HOSBX34	706769	815	389 - 547	1838		L0439: 2, S0003: 1 and L0438: 1.		
HOSBR53	728525	816	11 - 208	1839	Ser-8 to Ser-19, Lys-26 to Glu-31, Gln-55 to Cys-64.	S0003: 1 and L0439: 1.		
HOSBO34	706770	817	1 - 99	1840	Thr-1 to Arg-14.	S0003: 1, L0779: 1 and L0589: 1.		
HOSBM55	732550	818	269 - 541	1841	Lys-40 to Thr-45.	L0748: 3 and S0003: 1.		
HOSAY52	728759	819	2 - 154	1842	Leu-29 to Thr-34.	L0756: 2 and S0003: 1. 14		
HOSAX03	960942	820	48 - 812	1843		L0758: 3 and S0003: 1.		
HOSAL10	968710	821	3 - 206	1844	Ala-17 to Asn-22, Pro-24 to Gln-30.	S0003: 1 and L0362: 1.		
HOSAI41	712708	822	859 - 1077	1845	Cys-1 to Gly-6, Gln-26 to Leu-45.	L0748: 3, L0749: 2 and S0003: 1.		
HOSAH30	693406	823	312 - 491	1846		S0003: 1 and L0439: 1.		
HOSAF19	672078	824	124 - 267	1847	Ser-14 to Lys-21, Tyr-33 to Ile-39.	S0003: 1 and L0596: 1.		
HOHEN28	686034	825	2 - 232	1848		L0794: 6, L0768: 2, L0740: 2, L0777: 2, S0250: 1, L0764: 1, L0766: 1, L0655: 1 and L0758: 1.		

HOHEG71	760051	826	262 - 420	1849	Ser-11 to Ser-31, Thr-46 to His-53.	L0777: 2 and S0250: 1.		
HOHDF94	793970	827	456 - 671	1850		S0250: 1 and L0594: 1.		
HOHCV57	734413	828	66 - 380	1851	Phe-2 to Lys-7, Ser-38 to Arg-44, Gly-71 to Asn-94.	S0250: 1 and L0748: 1.		
HOHCL29	634778	829	257 - 6	1852	Asp-7 to Gly-12.	AR054: 9, AR051: 3, AR050: 2 S0250: 1		
HOHCH52	588375	830	2 - 181	1853	Lys-1 to Tyr-8, Lys-10 to Lys-16.	S0250: 1 and L0754: 1.		
HOHCG79	859029	831	1 - 156	1854	Asn-47 to Trp-52.	S0250: 1 and L0763: 1.		
HOHCD58	973105	832	101 - 373	1855	Glu-8 to Pro-14.	S0250: 1		
HOHBZ27	588364	833	203 - 376	1856		S0250: 1, L0435: 1 and L0439: 1.		
HOHBY26	588358	834	3 - 476	1857	Asp-32 to Asn-38, His-116 to Asn-122, Phe-125 to Met-130.	S0250: 1 and L0591: 1.		
HOHBV67	718562	835	3 - 179	1858	Pro-19 to Asn-27, Tyr-46 to His-51.	S0250: 1, L0731: 1, L0597: 1 and L0589: 1.		
HOHBS10	964324	836	157 - 408	1859		S0250: 1 and L0758: 1.		
HOHBP36	708158	837	416 - 141	1860	Ser-12 to Cys-17, Lys-74 to Gly-83.	L0748: 4 and S0250: 1.		
HOHBN56	859041	838	2 - 208	1861	Asn-46 to Leu-51.	L0766: 4 and S0250: 1.		
HOHBL35	973238	839	62 - 256	1862	Ile-23 to Phe-32, Leu-40 to Ala-47.	S0250: 1		
HOHBI84	782908	840	62 - 376	1863	Gly-1 to His-6, Pro-19 to Pro-36,	S0250: 1 and L0742: 1. 9q		

HOHBB90	588308	841	300 - 434	1864	Ser-38 to Ser-46.	S0250: 1 and L0754: 1. 17q25	114290, 138033, 162100, 170500, 170500, 170500, 180860, 264470
HOHAV60	489007	842	96 - 668	1865		S0250: 1, L0748: 1 and L0740: 1.	
HOHAT59	867949	843	2 - 214	1866	Ala-58 to Tyr-66.	S0250: 1 and L0370: 1.	
HOHAT11	966727	844	114 - 473	1867	Lys-37 to Tyr-47.	L0180: 1 and S0250: 1.	
HOHAQ65	859057	845	15 - 209	1868		S0250: 1 and L0748: 1.	
HOHAM66	859058	846	1 - 522	1869	Gln-94 to Met-101, Thr-109 to Gly-124, Gln-149 to Gly-155.	L0754: 2 and S0250: 1. 17q12	144200, 148066, 148066, 148067, 148067, 148069, 154275, 180240, 182138, 600119, 600119, 600881, 601363, 601687, 601954
HOHAI11	947140	847	1510 - 2127	1870	Phe-22 to Lys-30, Glu-122 to Ser-127, Arg-183 to Lys-190.	S0250: 1	
	965035	1026	338 - 117	2049			
	966030	1027	332 - 490	2050			
HOHAE76	494001	848	94 - 309	1871		S0250: 1	
	859064	1028	156 - 344	2051			
HOEOA28	859156	849	521 - 739	1872	Gly-46 to Gly-51.	L0731: 2, L0763: 1, L0766: 1 and S0126: 1.	
HOENH06	934095	850	1 - 201	1873	Asp-24 to Ala-32.	L0438: 3, L0439: 3,	

HOELI08	958181	851	413 - 138	1874			S0126: 1, L0743: 1, L0747: 1, L0749: 1, L0750: 1 and L0758: 1.		
HOEX37	708728	852	553 - 717	1875			L0766: 2, L0769: 1, L0800: 1, L0803: 1, L0804: 1 and S0126: 1.		
HOEEU57	932562	853	1 - 738	1876	Gly-1 to Arg-15.		L0744: 2, S0126: 1 and L0747: 1.		
HOER75	767265	854	278 - 463	1877			AR089: 30, AR061: 7 L0774: 1, S0126: 1 and L0780: 1.		
HOECJ59	739426	855	1 - 462	1878	Cys-1 to Ala-7, Glu-16 to Gly-21, Arg-24 to Gln-30, Ser-41 to Met-52, Trp-75 to His-82.		L0756: 2 and S0126: 1. L0750: 2 and S0126: 1.		
HOECF70	573426	856	39 - 161	1879			S0126: 1		
HOEBT89	921065	857	215 - 364	1880			S0126: 1 and L0754: 1.		
HOACG06	954572	858	88 - 252	1881			L0747: 2, H0252: 1 and L0439: 1.		
HOABY40	711510	859	248 - 466	1882			H0252: 1 and L0756: 1.		
HOABX26	753954	860	93 - 275	1883			H0252: 1, L0769: 1, L0375: 1, L0748: 1 and L0749: 1.		
HOABX21	531390	861	3 - 89	1884	Thr-2 to Lys-18.		H0252: 1		
HOABW12	968797	862	11 - 244	1885	Pro-2 to Ala-7.		H0252: 1 and L0749:		

HOABG91	811156	863	1 - 234	1886	Asp-22 to Ser-27, Asn-29 to Glu-40, His-56 to Gly-73.	1.	H0252: 1	11p11.2- p12	133701, 168500, 171650, 176930, 176930, 600623, 600811, 600958
HOABF65	888203	864	149 - 298	1887			AR050: 12, AR051: 10, AR054: 7 H0252: 1		
HOABD07	954060	865	156 - 344	1888	Ser-15 to Gly-20, Ala-26 to Tyr-33.	1.	H0252: 1 and L0777:		
HOABA95	796063	866	101 - 316	1889	Lys-8 to Gln-14, Ile-27 to Thr-52.	1.	H0252: 1 and L0754:		
HOAAX37	708718	867	108 - 242	1890		1.	H0252: 1 and L0748:		
HOAAW11	967660	868	207 - 395	1891	Leu-1 to Trp-6.	1.	H0252: 1 and L0527:		
HOAAW02	920869	869	108 - 329	1892	Thr-1 to Asn-12, Gly-18 to Phe-24, Cys-40 to Trp-45, Thr-50 to His-58.	1.	H0252: 1 and L0766:		
HOAAV77	772512	870	154 - 378	1893	Cys-30 to Arg-38.	1.	L0740: 2 and H0252:		
HOAAO86	859626	871	198 - 443	1894	Pro-18 to Arg-42, Asn-55 to Ala-60.		H0252: 1		
HOAAM67	751947	872	108 - 290	1895	Asp-24 to Pro-31.	1.	H0252: 1 and L0748:		
HOAAK71	761445	873	156 - 389	1896	Thr-18 to Lys-25.	1.	H0252: 1 and L0748:		

HOAAK11	859624	874	1 - 396	1897	Gly-30 to Glu-44, Ser-51 to Glu-56, Arg-91 to Asn-99, Pro-101 to Gly-108, Pro-117 to Leu-122.	H0252: 1		
HOAAI58	859643	875	104 - 238	1898		H0023: 4, L0759: 2, H0252: 1, L0740: 1 and L0596: 1.		
HOAAH77	772514	876	2 - 211	1899	Arg-16 to Ser-23.	H0252: 1 and L0747: 1.		
HOAAH41	712601	877	106 - 246	1900	Ser-9 to Arg-17, Phe-24 to Leu-33.	H0252: 1, L0748: 1 and L0749: 1.		
HMUBZ11	966856	878	161 - 316	1901	Gln-45 to Pro-52.	H0023: 1, H0529: 1 and L0748: 1.		
HMUBY48	721586	879	50 - 154	1902	Ser-8 to Glu-13, Lys-20 to Lys-31.	H0529: 1		
HMUBY20	669581	880	197 - 361	1903	Pro-23 to Asn-29.	H0529: 1		
HMUBV40	837969	881	3 - 434	1904	Tyr-70 to Ser-81, Arg-87 to Arg-97.	H0529: 1		
HMUBR94	793261	882	265 - 450	1905	Leu-10 to Phe-15.	H0529: 1		
HMUBR78	955060	883	75 - 518	1906	Pro-9 to Pro-17, Asp-24 to Glu-30, Asn-65 to Ser-75.	H0529: 1 and L0745: 1.		
HMUBQ01	918052	884	29 - 214	1907	Cys-6 to Val-13, Cys-57 to Asn-62.	H0529: 1		
HMUBP74	765502	885	380 - 553	1908	Ala-1 to His-6.	H0529: 1		
HMUBP38	716800	886	30 - 206	1909		H0529: 1		
HMUBN15	659543	887	258 - 40	1910	Pro-14 to Lys-23.	H0529: 1		

HMUBN05	932057	888	248 - 439	1911			H0529: 1		
HMUBM89	786082	889	458 - 309	1912			H0529: 1		
HMUBM85	784295	890	86 - 229	1913			H0529: 1		
HMUBM23	675296	891	2 - 319	1914		Pro-41 to Ala-47, Arg-50 to Gly-58.	L0439: 3, H0529: 1 and L0438: 1.		
HMUBM21	861218	892	316 - 525	1915			H0529: 1		
HMUBM01	916291	893	1 - 429	1916		Pro-11 to Gly-16, Ser-35 to Gly-55, Gln-63 to Leu-68, Asp-118 to Ser-123, Arg-136 to Ala-141.	H0529: 1 and L0601: 1.		
HMUBL79	774904	894	110 - 229	1917		Gly-15 to Lys-20, Ile-25 to Leu-30.	H0529: 1		
HMUBL25	678011	895	109 - 291	1918		Glu-19 to Arg-25.	H0529: 1 and L0748: 1.		
HMUBI26	424764	896	3 - 209	1919		Lys-6 to Asp-14, Lys-22 to Cys-27.	L0439: 2 and H0529: 1.		
HMUBH84	782971	897	33 - 251	1920		Thr-19 to Thr-28, Ser-43 to Gly-54, Asp-67 to Gly-73.	H0529: 1 and L0749: 1.		
HMUBC76	769968	898	260 - 415	1921		Gly-15 to Ile-21, Ser-24 to Ser-32.	H0529: 1 and L0748: 1.		
HMUBA75	767192	899	214 - 375	1922		Asn-12 to Asn-25.	H0529: 1		
HMUBA61	741710	900	56 - 172	1923			H0529: 1		
HMUAT71	772958	901	1 - 264	1924		Ser-15 to Asp-22, Arg-28 to Arg-35.	H0529: 1 and L0601: 1.	6	
HMUAE85	783543	902	41 - 259	1925			H0529: 1 and L0731: 1.		

HFOZC29	923288	903	500 - 195	1926	Cys-2 to Asp-8, Ser-59 to Gly-65.	L0384: 1, L0809: 1, L0731: 1 and S0276: 1.		
HFOZA47	909372	904	110 - 262	1927	Ser-26 to Cys-31.	L0748: 1 and S0276: 1.		
HFOYW76	769894	905	129 - 401	1928	Gln-19 to Cys-28.	L0439: 1 and S0276: 1.		
HFOYV08	959038	906	73 - 255	1929	Leu-2 to Arg-8, Lys-42 to Ile-47.	L0021: 1, L0769: 1, L0794: 1, L0803: 1, L0527: 1, L0731: 1, L0758: 1 and S0276: 1.		
HFOYS58	735816	907	134 - 280	1930	Val-10 to Pro-20.	L0589: 1 and S0276: 1.		
HFOYN65	747740	908	3 - 167	1931	Gln-1 to Thr-12.	L0439: 3 and S0276: 1.		
HFOYN01	854780	909	242 - 406	1932		L0591: 1 and S0276: 1.		
HFOYM48	721455	910	64 - 279	1933		L0598: 2, L0766: 1, L0805: 1, L0777: 1 and S0276: 1.		
HFOYL33	702209	911	95 - 508	1934	Ser-1 to Ser-6, Asp-24 to Ala-36, Arg-130 to Leu-135.	L0640: 1, L0748: 1 and S0276: 1.		
HFOYK21	670653	912	28 - 180	1935	Glu-21 to Glu-29, Asn-33 to Tyr-39.	L0758: 2, L0779: 1 and S0276: 1.		
HFOYK02	919458	913	3 - 140	1936		L0750: 2 and S0276: 1.		
HFOYJ30	932485	914	42 - 299	1937		L0747: 1 and S0276: 1.		
HFOYH01	916055	915	259 - 432	1938	Thr-4 to Lys-17, Ser-35 to Gly-40, Thr-44 to Cys-52.	L0761: 1, L0803: 1, L0774: 1, L0775: 1, L0599: 1 and S0276: 1.		
HFOYG88	494875	916	463 - 765	1939		L0747: 3 and S0276: 1.		
HFOYG86	949496	917	220 - 62	1940	Pro-19 to Lys-25, Phe-37 to Asn-44.	AR050: 13, AR054: 7, AR089: 3, AR051: 2, AR061: 1		

	955554	1029	245 - 760					L0777: 2, L0731: 2, L0659: 1 and S0276: 1.		
HFOYC08	958975	918	209 - 364	1941	2052	Arg-27 to Gly-35, Tyr-72 to Lys-78, Phe-108 to Lys-114.		L0770: 1 and S0276: 1.		
HFOYA17	662642	919	94 - 348	1942		Arg-32 to Pro-41, Pro-43 to Gly-50.		L0740: 1 and S0276: 1.		
HFOXW67	494854	920	264 - 485	1943		Gln-29 to Asn-37, Lys-55 to Gln-64.		L0439: 1 and S0276: 1.		
HFOXV94	794175	921	2 - 322	1944		Pro-3 to Arg-10, Pro-12 to Arg-18.		L0592: 1 and S0276: 1.		
HFOXT74	875383	922	281 - 535	1945		Ala-31 to Gly-38.		L0749: 1 and S0276: 1.		
HFOXT35	707088	923	143 - 325	1946				S0276: 1		
HFOXSA2	713514	924	352 - 110	1947		Ser-45 to Lys-55.		S0276: 1		
HFOXO57	928171	925	1 - 507	1948		Pro-5 to Gln-14, Lys-26 to Cys-32, Tyr-58 to Gln-69, Gly-78 to Gly-84, Lys-93 to Leu-117.		L0439: 1, L0756: 1 and S0276: 1.		
HFOXO33	702212	926	311 - 493	1949		Asp-32 to Asn-41.		L0623: 1, L0646: 1, L0748: 1 and S0276: 1.		
HFOXM53	587972	927	333 - 560	1950				L0748: 1 and S0276: 1.		
HFOXL88	909839	928	90 - 425	1951		Lys-5 to Ser-12, Thr-17 to Ser-24.		L0562: 1 and S0276: 1.	7q22- q31.1	126650, 126650, 150240, 154276, 173360, 173360, 180105, 222800, 246900, 602136,

[illegible]

HFITYA08	962212	944	191 - 421	1967		Thr-6 to Lys-13, Phe-37 to His-45, Ala-58 to Ser-72.	L0756: 1, L0752: 1, L0731: 1 and S0242: 1.		
HFIXZ95	915703	945	2 - 208	1968		Val-2 to Ser-14.	L0589: 1 and S0242: 1.		
HFIXZ19	683033	946	613 - 410	1969			L0608: 1 and S0242: 1.		
HFIXR93	894013	947	242 - 460	1970			L0758: 1 and S0242: 1.		
HFIXR68	752858	948	220 - 342	1971			L0740: 2 and S0242: 1.		
HFIXP31	697759	949	3 - 317	1972		Leu-9 to Asn-16, Thr-92 to Pro-100.	L0748: 1 and S0242: 1.		
HFIXP04	839910	950	185 - 400	1973		Ser-31 to Glu-36, Lys-44 to Cys-51.	AR089: 4, AR061: 1 L0777: 3, L0809: 1 and S0242: 1.		
HFIXJ53	489122	951	94 - 348	1974			L0779: 1 and S0242: 1.		
HFIXB77	772116	952	137 - 352	1975			L0748: 1 and S0242: 1.		
HFIVS81	387591	953	2 - 157	1976			L0754: 1 and S0242: 1.		
HFIVS21	855131	954	1 - 279	1977			L0439: 1 and S0196: 1.		
HFIVS08	959272	955	115 - 255	1978		Pro-1 to Ser-6.	L0545: 1 and S0196: 1.		
HFUIZ63	745033	956	74 - 283	1979		Ser-12 to Gly-17.	L0021: 1 and S0196: 1.		
HFUIY49	855133	957	65 - 382	1980		Leu-10 to Lys-22, Ser-46 to Ala-54, Pro-85 to Phe-91.	L0748: 1 and S0196: 1.		
HFUIV58	735350	958	2 - 205	1981			S0196: 1		
HFUIV18	787095	959	3 - 248	1982			L0740: 2, L0747: 2 and S0196: 1.		
HFUIM33	702319	960	214 - 372	1983			L0746: 1 and S0196: 1.		
HFUIH65	747836	961	34 - 183	1984		Leu-7 to Cys-14,	S0196: 1		
							L0752: 2, L0740: 1,		

						Pro-16 to Ser-24, Gln-43 to His-50.	L0745: 1 and S0196: 1.		
HFIUD47	720254	962	129 - 380	1985			L0750: 2, L0747: 1, L0731: 1, L0591: 1 and S0196: 1.		
HFIU46	718078	963	295 - 672	1986			L0745: 1, L0746: 1 and S0196: 1.		
HFIUG36	707883	964	1 - 183	1987		Ser-1 to Asp-9.	L0749: 1 and S0194: 1.		
HFIUG20	669580	965	307 - 435	1988			L0748: 1 and S0194: 1.		
HFIUF58	735927	966	214 - 492	1989		Lys-1 to Lys-15, Arg-22 to Arg-31, Thr-68 to Pro-73, Pro-79 to Ser-86.	L0777: 2 and S0194: 1.		
HFIUZ92	494044	967	170 - 3	1990		Asp-1 to Cys-6, Lys-15 to Phe-23, Asn-46 to Arg-56.	S0194: 1		
	533295	1030	1 - 843	2053		Gly-1 to Val-7, Gln-28 to Thr-34, Ala-100 to Thr-108, Ser-115 to Arg-122, Ser-156 to Glu-162, Ser-174 to Tyr-186, Glu-188 to Phe-193.			
HFIU85	793332	968	242 - 526	1991			L0598: 1 and S0194: 1.		
HFIUR63	744994	969	312 - 467	1992		Ala-6 to Ile-12.	L0439: 3 and S0194: 1.		
HFIIL37	561375	970	3 - 350	1993		Ser-1 to Gly-18, Gly-27 to Leu-39, Ser-76 to Thr-89.	AR050: 241, AR051: 230, AR054: 157 S0194: 1		

HFIHK75	767222	971	541 - 810	1994	Trp-1 to Val-6, His-20 to Ser-28, Arg-47 to Pro-53, Thr-65 to Pro-71, Ser-78 to Gly-90.	L0439: 2, L0777: 2 and S0194: 1.		
HFIHK32	424259	972	133 - 321	1995	His-5 to Thr-10.	L0754: 1 and S0194: 1.		
HFIHK07	953034	973	84 - 317	1996		L0663: 1 and S0194: 1.		
HFIHJ14	839523	974	429 - 707	1997	Val-17 to His-33, Arg-51 to Leu-60, Leu-85 to Pro-93.	AR054: 62, AR050: 59, AR051: 58 S0194: 1		
HFIHW91	907618	975	3 - 527	1998	Trp-5 to Pro-11.	AR089: 13, AR061: 6 L0779: 1, L0780: 1, L0759: 1 and S0194: 1.		
HFIHW16	858594	976	3 - 272	1999	Gln-22 to Trp-27.	L0744: 1 and S0194: 1.		
HFIHW11	947856	977	22 - 201	2000		L0527: 2 and S0194: 1.		
HFIHV56	470954	978	70 - 378	2001	Ser-1 to Arg-7.	L0592: 1 and S0194: 1.		
HFIHU76	769948	979	133 - 246	2002		L0748: 1 and S0194: 1.		
HFIHS86	785419	980	146 - 325	2003		L0598: 1 and S0194: 1.		
HFIHR78	773512	981	249 - 407	2004		L0745: 1 and S0194: 1.		
HFIHN35	707075	982	327 - 560	2005		L0748: 3, L0749: 1 and S0194: 1.		
HFIHK29	855174	983	97 - 450	2006	Val-3 to Arg-11, Pro-34 to His-47, Ser-58 to Leu-68, Pro-72 to Trp-77.	L0731: 2 and S0194: 1.		
HFIHF53	728259	984	369 - 500	2007	Ile-7 to Ile-13.	L0754: 1 and S0194: 1.		
HFIHD20	669731	985	3 - 338	2008	Arg-6 to Thr-11, Gly-27 to Leu-33,	L0605: 1 and S0194: 1.		

							Lys-52 to Phe-61, Gln-86 to Lys-92, Asn-102 to Arg-112.				
HFIDL68	928475	986	2 - 529	2009			Glu-40 to Lys-46, Phe-120 to Ser-132.			AR089: 7, AR061: 4, AR050: 2, AR054: 2, AR051: 1 S0192: 1	
HFIDL06	837524	987	50 - 487	2010			Val-1 to Gly-8, Gln-48 to Asp-53, Glu-61 to Asp-68, Val-88 to Lys-96, Asp-102 to Lys-108.			L0602: 1 and S0192: 1.	
HFIBK83	939556	988	2 - 502	2011			Val-48 to Pro-56, Asp-58 to Gln-69.			L0439: 1 and S0192: 1.	
HFIA X78	773445	989	80 - 217	2012						S0192: 1	
HFIA S49	722728	990	357 - 611	2013			Leu-5 to Lys-11.			L0740: 1 and S0192: 1.	
HFIA L66	587837	991	339 - 515	2014						L0740: 1 and S0192: 1.	
HCOKA10	907080	992	605 - 171	2015			Phe-13 to Thr-22.			AR054: 7, AR061: 2, AR089: 1, AR051: 1 H0636: 1	
	918918	1031	1663 - 1220	2054							
	919869	1032	1 - 396	2055			Pro-1 to Ser-9, Asp-127 to Asn-132.				
HCDEL02	920831	993	167 - 292	2016						H0251: 1 and L0776: 1.	
HCDDZ69	522220	994	198 - 341	2017						H0251: 1	
HCDDY54	529265	995	23 - 148	2018			Gln-12 to Asp-26.			H0251: 1	

HCDDO80	778563	996	85 - 402	2019	Tyr-8 to Thr-15.	H0251: 1 and L0596: 1.		
HCDCD64	863415	997	23 - 301	2020	Asp-35 to Cys-43.	H0251: 1 and L0740: 1.		
HCDBW41	712648	998	2 - 217	2021	Pro-2 to Lys-7.	L0439: 3 and H0251: 1.		
HCDBO86	784617	999	279 - 509	2022	Thr-62 to Asn-69, Cys-71 to Glu-77.	H0251: 1, L0747: 1, L0756: 1 and L0777: 1.		
HCDAO39	704504	1000	3 - 260	2023		H0251: 1 and L0588: 1.		
HCDA68	753814	1001	412 - 576	2024	Ala-3 to Thr-9, Arg-16 to Pro-23.	H0251: 1 and L0748: 1.		
HBSAP57	531874	1002	298 - 474	2025	Ser-1 to Gly-11, Pro-42 to Lys-54.	AR051: 87, AR054: 84, AR050: 83 H0381: 1		
	533619	1033	392 - 216	2056	Ser-1 to Gly-11, Pro-42 to Lys-54.			
HBCKF23	675613	1003	168 - 425	2026	Gly-9 to His-18.	L0758: 3, S0336: 1 and L0779: 1.		
HBCGD25	677689	1004	97 - 240	2027	Leu-39 to Lys-46.	L0748: 3 and S0334: 1.		
HAOAE95	795674	1005	95 - 217	2028	Gly-12 to Pro-20.	L0605: 2 and S0314: 1.		
HAOAD27	848729	1006	90 - 335	2029		S0314: 1 and L0747: 1.		
HANKG10	963926	1007	34 - 237	2030	Cys-1 to Phe-6, Leu-30 to Gly-38.	S0318: 1, L0766: 1 and L0803: 1.		
HANKB13	827062	1008	2 - 436	2031	Lys-4 to Gln-16, Lys-32 to Lys-39, Met-43 to Asn-48, Gln-70 to Leu-76.	S0318: 1, L0766: 1 and L0666: 1.		

HAMAC79	872774	1009	337 - 867	2032		AR089: 20, AR061: 13 H0122: 1		
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- [058] The first column in Table 1A provides a unique "Clone ID NO:Z" for a cDNA clone related to each contig sequence disclosed in Table 1A. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig, and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods known in the art and/or as described elsewhere herein.
- [059] The second column in Table 1A provides a unique "Contig ID" identification for each contig sequence. The third column provides the "SEQ ID NO:X" identifier for each of the musculoskeletal system associated contig polynucleotide sequences disclosed in Table 1A. The fourth column, "ORF (From-To)", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred open reading frame (ORF) shown in the sequence listing and referenced in Table 1A, column 5, as SEQ ID NO:Y. Where the nucleotide position number "To" is lower than the nucleotide position number "From", the preferred ORF is the reverse complement of the referenced polynucleotide sequence.
- [060] The fifth column in Table 1A provides the corresponding SEQ ID NO:Y for the polypeptide sequence encoded by the preferred ORF delineated in column 4. In one embodiment, the invention provides an amino acid sequence comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by "ORF (From-To)". Also provided are polynucleotides encoding such amino acid sequences and the complementary strand thereto.
- [061] Column 6 in Table 1A lists residues comprising epitopes contained in the polypeptides encoded by the preferred ORF (SEQ ID NO:Y), as predicted using the algorithm of Jameson and Wolf, (1988) Comp. Appl. Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). In specific embodiments, polypeptides of the invention comprise, or alternatively consist of, at least one, two, three, four, five or more of the predicted epitopes as described in Table 1A. It will be appreciated that depending on

the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly.

[062] Column 7 in Table 1A provides an expression profile and library code: count for each of the contig sequences (SEQ ID NO:X) disclosed in Table 1A, which can routinely be combined with the information provided in Table 4 and used to determine the normal or diseased tissues, cells, and/or cell line libraries which predominantly express the polynucleotides of the invention. The first number in column 7 (preceding the colon), represents the tissue/cell source identifier code corresponding to the code and description provided in Table 4. For those identifier codes in which the first two letters are not "AR", the second number in column 7 (following the colon) represents the number of times a sequence corresponding to the reference polynucleotide sequence was identified in the tissue/cell source. Those tissue/cell source identifier codes in which the first two letters are "AR" designate information generated using DNA array technology. Utilizing this technology, cDNAs were amplified by PCR and then transferred, in duplicate, onto the array. Gene expression was assayed through hybridization of first strand cDNA probes to the DNA array. cDNA probes were generated from total RNA extracted from a variety of different tissues and cell lines. Probe synthesis was performed in the presence of ^{33}P dCTP, using oligo(dT) to prime reverse transcription. After hybridization, high stringency washing conditions were employed to remove non-specific hybrids from the array. The remaining signal, emanating from each gene target, was measured using a Phosphorimager. Gene expression was reported as Phosphor Stimulating Luminescence (PSL) which reflects the level of phosphor signal generated from the probe hybridized to each of the gene targets represented on the array. A local background signal subtraction was performed before the total signal generated from each array was used to normalize gene expression between the different hybridizations. The value presented after "[array code]:" represents the mean of the duplicate values, following background subtraction and probe normalization. One of skill in the art could routinely use this information to identify normal and/or diseased tissue(s) which show a predominant expression pattern of the corresponding polynucleotide of the invention or to identify polynucleotides which show predominant and/or specific tissue and/or cell expression. The sequences disclosed herein have been determined to be predominantly expressed in

musculoskeletal system tissues, including normal and diseased musculoskeletal system tissues (See Table 1A, column 7 and Table 4).

[063] Column 8 in Table 1A provides a chromosomal map location for certain polynucleotides of the invention. Chromosomal location was determined by finding exact matches to EST and cDNA sequences contained in the NCBI (National Center for Biotechnology Information) UniGene database. Each sequence in the UniGene database is assigned to a "cluster"; all of the ESTs, cDNAs, and STSs in a cluster are believed to be derived from a single gene. Chromosomal mapping data is often available for one or more sequence(s) in a UniGene cluster; this data (if consistent) is then applied to the cluster as a whole. Thus, it is possible to infer the chromosomal location of a new polynucleotide sequence by determining its identity with a mapped UniGene cluster.

[064] A modified version of the computer program BLASTN (Altshul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)) was used to search the UniGene database for EST or cDNA sequences that contain exact or near-exact matches to a polynucleotide sequence of the invention (the 'Query'). A sequence from the UniGene database (the 'Subject') was said to be an exact match if it contained a segment of 50 nucleotides in length such that 48 of those nucleotides were in the same order as found in the Query sequence. If all of the matches that met this criteria were in the same UniGene cluster, and mapping data was available for this cluster, it is indicated in Table 1A under the heading "Cytologic Band". Where a cluster had been further localized to a distinct cytologic band, that band is disclosed; where no banding information was available, but the gene had been localized to a single chromosome, the chromosome is disclosed.

[065] Once a presumptive chromosomal location was determined for a polynucleotide of the invention, an associated disease locus was identified by comparison with a database of diseases which have been experimentally associated with genetic loci. The database used was the Morbid Map, derived from OMIM™ (*supra*). If the putative chromosomal location of a polynucleotide of the invention (Query sequence) was associated with a disease in the Morbid Map database, an OMIM reference identification number was noted in column 9, Table 1A, labeled

“OMIM Disease Reference(s)”. Table 5 is a key to the OMIM reference identification numbers (column 1), and provides a description of the associated disease in Column 2.

TABLE 1B

Clone ID NO:Z	SEQ ID NO:X	CONTIG ID:	BAC ID: A	SEQ ID NO:B	EXON From-To
HANGA63	11	927404	AL133312	2057	1-333
HANGA63	11	927404	AL135752	2058	1-333
HANGA63	11	927404	AL133312	2059	1-467
HANGA63	11	927404	AL135752	2060	1-467
HANGA69	12	718174	AL353590	2061	1-446
HANGA85	13	746265	AC007705	2062	1-330
HANGA92	14	791182	AL359257	2063	1-167
HANGA92	14	791182	AL359257	2064	1-825 1179-1523 1777-2115
HANGC05	15	674059	AC024377	2065	1-119
HANGC05	15	674059	AC018496	2066	1-119
HANGC05	15	674059	AC024377	2067	1-202
HANGC05	15	674059	AC018496	2068	1-187
HANGC30	18	966430	AC022618	2069	1-408
HANGC33	19	702072	AC069127	2070	1-272
HANGC84	21	715991	AL137178	2071	1-1034 1132-1714
HANGC84	21	715991	AC016847	2072	1-1034 1132-1714
HANGF36	22	952583	AC013496	2073	1-255
HANGF36	22	952583	AC013496	2074	1-616
HANGF49	23	722635	AC013465	2075	1-469
HANGF49	23	722635	AC026298	2076	1-123
HANGF49	23	722635	AC016911	2077	1-469
HANGF49	23	722635	AC016749	2078	1-123
HANGF49	23	722635	AC010080	2079	1-469
HANGF49	23	722635	AC006386	2080	1-469
HANGF49	23	722635	AC026298	2081	1-399
HANGF49	23	722635	AC016749	2082	1-399
HANGG22	24	848727	AL355112	2083	1-374
HANGG22	24	848727	AL355112	2084	1-147
HANGH48	25	718759	AC069530	2085	1-378
HANGH48	25	718759	AC069530	2086	1-509
HANGH53	26	727914	AC073319	2087	1-440
HANGH66	28	661513	AC036194	2088	1-457
HANGH66	28	661513	AC026013	2089	1-457
HANGH66	28	661513	AC025534	2090	1-457

HANKD09	29	625167	AC012521	2091	1-409
HANKD09	29	625167	AC027666	2092	1-409
HANKD47	30	719963	AL355592	2093	1-464
HANKD83	31	963964	AC068969	2094	1-316
HANKD83	31	963964	AC067805	2095	1-316
HANKG78	32	710760	AC006514	2096	1-385 594-1524 1793-2194 4246-4590 4888-5238
HANKG78	32	710760	AC006510	2097	1-931 1200-1601
HANKG78	32	710760	AC006510	2098	1-379
HANKG90	33	746282	AP001644	2099	1-437
HANKG90	33	746282	AC021506	2100	1-437
HANKH48	34	721340	AP001203	2101	1-382
HANKH56	35	733063	AC074293	2102	1-417
HANKH56	35	733063	AC068194	2103	1-417
HAOAA78	37	756979	AC008945	2104	1-549
HAOAA78	37	756979	AC008945	2105	1-481
HAOAA90	38	919249	AC044917	2106	1-348
HAOAA90	38	919249	AP001839	2107	1-332
HAOAA90	38	919249	AC023090	2108	1-348
HAOAA90	38	919249	AC018445	2109	1-348
HAOAA90	38	919249	AC044917	2110	1-887
HAOAA90	38	919249	AP001839	2111	1-146 303-921
HAOAA90	38	919249	AC023090	2112	1-887
HAOAC05	39	932017	AC008279	2113	1-516
HAOAC05	39	932017	AC008279	2114	1-478
HAOAH38	45	705946	AC005036	2115	1-345
HAOMA13	46	915881	AC068969	2116	1-368
HAOMA13	46	915881	AC067805	2117	1-368
HAOMA13	46	915881	AC067805	2118	1-536
HAOMB64	47	960293	AC019144	2119	1-1138
HAOMB64	47	960293	AC019144	2120	1-319
HAOMB64	47	960293	AC019144	2121	1-455
HAOMC21	48	670518	AL354920	2122	1-788
HAOMC21	48	670518	AL354920	2123	1-317
HAOMC21	48	670518	AL354920	2124	1-1979 3907-4540 5067-5184 6386-6845
HAOME45	50	705947	AP001011	2125	1-1739
HAOME45	50	705947	AP000937	2126	1-1738
HAOME45	50	705947	AP000898	2127	1-1738

					1771-4394
HAOME45	50	705947	AC015958	2128	1-1739 1772-4400
HAOME45	50	705947	AP000937	2129	1-415 436-874
HAOME45	50	705947	AP001011	2130	1-415 436-874
HAOME45	50	705947	AP000898	2131	1-415 436-874
HAOME45	50	705947	AP000937	2132	1-665
HAOME45	50	705947	AC015958	2133	1-414 435-873
HBCKE22	54	674041	AC016659	2134	1-562 827-886 4639-5057 6461-6525 6654-7045 7193-7882 8357-8477 11540-11583 11943-12257 13444-13934 14354-14528 15155-15287
HBCKE22	54	674041	AC012481	2135	1-691
HBCKE22	54	674041	AC016659	2136	1-258
HBCKE22	54	674041	AC012481	2137	1-121 3184-3224 3587-3901 5088-5578 5998-6172 6799-6931
HBCKE22	54	674041	AC012481	2138	1-392
HBSAK76	57	506666	AC027632	2139	1-349
HBSAK76	57	506666	AC027632	2140	1-425
HBSAL69	58	573004	AC020791	2141	1-433
HBSAL80	59	506580	AC018712	2142	1-380
HBSAL80	59	506580	AC074334	2143	1-125
HBSAL80	59	506580	AC026718	2144	1-420
HBSAP02	62	920648	AC022496	2145	1-490
HBSAP02	62	920648	AC025456	2146	1-130 236-725 796-1013 2665-2751 3801-4267 5755-6475 7371-7547

					9209-9496 9611-10511 11152-11890 11984-12319 12651-12745 16691-17158 17236-17382 22177-22609
HBSAP02	62	920648	AC026437	2147	1-122 228-717 788-1005 2655-2741 3791-4257 5740-6460 7356-7532 9194-9481 9596-10496 11137-11875 11969-12304 12636-12730 16676-17143 17221-17367 22161-22574 29380-29520 36637-36948 37077-37558 38020-38322 39908-40220 41806-41890 42060-43287 43415-44248 44300-44584 44929-45056 45424-45902 46737-46932 47156-49997
HBSAP02	62	920648	AC022496	2148	1-218
HBSAP02	62	920648	AC026437	2149	1-751
HBSAP02	62	920648	AC026437	2150	1-934
HBSAQ64	64	530344	AC027573	2151	1-341
HBSAQ64	64	530344	AC073413	2152	1-341
HBSAQ64	64	530344	AC073413	2153	1-92
HBSDD91	67	775313	AC027644	2154	1-286 361-599 687-919 1726-2633
HBSDD91	67	775313	AC027644	2155	1-234

HCDAA94	68	661278	AC026053	2156	1-259
HCDAA94	68	661278	AC022262	2157	1-274
HCDAA94	68	661278	AL020995	2158	1-259
HCDAA94	68	661278	AC022262	2159	1-526
HCDAA94	68	661278	AL020995	2160	1-526
HCDAG92	74	724693	AP001105	2161	1-496
HCDAG92	74	724693	AP001900	2162	1-496
HCDAG92	74	724693	AP001145	2163	1-496
HCDAG95	75	533871	AC018891	2164	1-441
HCDAG95	75	533871	AC018891	2165	1-327
HCDAH34	76	533870	AC010469	2166	1-483
HCDAH34	76	533870	AC026718	2167	1-483
HCDAH34	76	533870	AC010469	2168	1-122
HCDAH34	76	533870	AC010469	2169	1-272
HCDAJ67	77	925362	AL049875	2170	1-317
HCDAJ67	77	925362	AL049875	2171	1-141
HCDAK93	78	523648	AC027474	2172	1-527
HCDAK93	78	523648	AC010332	2173	1-526
HCDAK93	78	523648	AC021112	2174	1-527
HCDAK93	78	523648	AC027474	2175	1-684
HCDAK93	78	523648	AC010332	2176	1-684
HCDAK93	78	523648	AC021112	2177	1-684
HCDAM34	80	523607	AC005969	2178	1-98 1380-1550
HCDAM34	80	523607	AC005969	2179	1-227
HCDAO32	81	530006	AC068780	2180	1-285
HCDAO32	81	530006	AC073907	2181	1-285
HCDAO32	81	530006	AC068780	2182	1-136
HCDAO32	81	530006	AC073907	2183	1-297
HCDAT56	82	533881	AL109657	2184	1-664 792-1138 1613-2026 6132-6234 6599-7035 7168-7446 8133-8262 8374-8670 8831-9478 9704-9762 9777-10137 10260-11201 11900-12541
HCDAT56	82	533881	AL109657	2185	1-489
HCDAT56	82	533881	AL109657	2186	1-369
HCDBO13	83	709590	AC007411	2187	1-323
HCDBR39	85	921893	AC008594	2188	1-409

HCDBR39	85	921893	AC040160	2189	1-410
HCDBR39	85	921893	AC008594	2190	1-761
HCDBR39	85	921893	AC008594	2191	1-1026
HCDBR39	85	921893	AC040160	2192	1-1026
HCDBR39	85	921893	AC040160	2193	1-761
HCDBU77	86	661272	AL121747	2194	1-400 540-929 957-1393 1904-2140 3206-3745 4498-4693 4849-5203 6468-6828 7645-8255 8418-8525 9502-10126
HCDBU77	86	661272	AL121747	2195	1-756
HCDBW51	87	556469	AL358472	2196	1-288
HCDBW51	87	556469	AL358472	2197	1-309
HCDBX78	89	847580	AC026340	2198	1-252
HCDBX78	89	847580	AC026340	2199	1-111
HCDCB84	90	670159	AL035634	2200	1-241
HCDCB84	90	670159	AL139330	2201	1-77 563-1013 1219-1674 2670-2885 4767-5013 5856-5969 6030-6407 6602-8576
HCDCB84	90	670159	AL035634	2202	1-451 657-1112
HCDCB84	90	670159	AL139330	2203	1-384
HCDCE62	92	523582	AL137065	2204	1-305
HCDCE62	92	523582	AL031177	2205	1-305
HCDCF11	93	967768	AC021163	2206	1-278
HCDCF11	93	967768	AC006942	2207	1-278
HCDCF11	93	967768	AC021163	2208	1-148 244-287 843-967
HCDCF11	93	967768	AC006942	2209	1-148 244-287 843-967
HCDCF11	93	967768	AC006942	2210	1-476 718-997
HCDCK91	95	592465	AC024885	2211	1-3448

HCDCR26	96	960048	AP000087	2212	1-429 732-1074 1121-1255 3513-3762
HCDCR26	96	960048	AP000139	2213	1-429 732-1074 1121-1255 3513-3762
HCDCR26	96	960048	AP000226	2214	1-429 732-1074 1121-1255 3513-3762
HCDCR26	96	960048	AP000226	2215	1-2571
HCDCR26	96	960048	AP000087	2216	1-2571
HCDCR26	96	960048	AP000139	2217	1-2571
HCDCX68	97	529778	AC003692	2218	1-44 153-684 695-1033 2881-3167 3597-8068 8150-9192
HCDCX68	97	529778	AC003692	2219	1-342
HCDCX68	97	529778	AC003692	2220	1-467
HCDDDB62	100	529890	AC015589	2221	1-570
HCDDDB62	100	529890	AC010328	2222	1-570
HCDDDB62	100	529890	AC015589	2223	1-340
HCDDDB62	100	529890	AC010328	2224	1-82 355-795 871-998 1300-1582 1629-2248 2727-2918 4474-4729 4876-6190 6240-9439
HCDDDB62	100	529890	AC010328	2225	1-340
HCDDI61	101	529937	AC005876	2226	1-428
HCDDI61	101	529937	AL358234	2227	1-428
HCDDI61	101	529937	AL161936	2228	1-428
HCDDI61	101	529937	AC005876	2229	1-247
HCDDI61	101	529937	AL358234	2230	1-247
HCDDI61	101	529937	AL161936	2231	1-247
HCDDU07	102	954177	AC005498	2232	1-1881
HCDDU07	102	954177	AC005498	2233	1-380
HCDDV90	103	847575	AC021553	2234	1-251
HCDDV90	103	847575	AC067837	2235	1-251

HCDDV90	103	847575	AC067837	2236	1-1510
HCDDV90	103	847575	AC067837	2237	1-450
HCDDY57	104	556465	AL354936	2238	1-273
HCDDY57	104	556465	AC021410	2239	1-273
HCDDY57	104	556465	AL354936	2240	1-186
HCDDY57	104	556465	AC021410	2241	1-153
HCDDZ09	105	523605	AC008866	2242	1-156
HCDDZ09	105	523605	AC016641	2243	1-156
HCDEB49	107	847572	AC024998	2244	1-242
HCDEB49	107	847572	AL390122	2245	1-242
HCDEB49	107	847572	AF198096	2246	1-242
HCDEB49	107	847572	AL390122	2247	1-430
HCDEB49	107	847572	AL390122	2248	1-419
HCDEB49	107	847572	AF198096	2249	1-430
HCDEB49	107	847572	AF198096	2250	1-500
HCDEB78	108	921710	AL359513	2251	1-300
HCDER16	111	667338	AC008064	2252	1-315
HCDER16	111	667338	AC008064	2253	1-415
HCDER16	111	667338	AC008064	2254	1-259
HCDER29	112	523506	AC022835	2255	1-203
HCDER29	112	523506	AC012476	2256	1-234 244-446 460-664 814-913 3082-3278 3691-4090
HCDER29	112	523506	AC022835	2257	1-155
HCDER29	112	523506	AC012476	2258	1-412
HCDET89	113	524045	AC009719	2259	1-323
HCDET89	113	524045	AC022939	2260	1-323
HCDET89	113	524045	AC009719	2261	1-138
HCDET89	113	524045	AC009719	2262	1-308
HCDET89	113	524045	AC022939	2263	1-138
HCDET89	113	524045	AC022939	2264	1-308
HFIAE82	116	779898	AC020669	2265	1-443
HFIAI07	118	952884	AC005722	2266	1-365 1763-1914 2765-3000 3766-3854 4573-5237 6312-7007 7152-7793 8026-8551 8938-9098 9770-10050 11976-12661

					12934-13016 13421-13727 14047-14140 14549-14721 15329-15864 16167-16198 21769-21933 22605-22741 22939-23176 24138-24261 24368-24492 26100-26500 26685-28818
HFIAP07	118	952884	AC005722	2267	1-491
HFIAP31	119	697775	AL360269	2268	1-291
HFIAP31	119	697775	AL356323	2269	1-374
HFIAP31	119	697775	AC004916	2270	1-374
HFIAP31	119	697775	AC004916	2271	1-480
HFIAP89	120	587844	AC013526	2272	1-343
HFIAP89	120	587844	AC011769	2273	1-342
HFIAP89	120	587844	AC011766	2274	1-342
HFIAP91	121	925831	AC002094	2275	1-282 780-1066 1693-1777 2672-3234 3779-3876 4254-4331 4547-4658 5768-5907 6777-6804 6988-7438 7930-8074 8084-8109 8407-8492 9334-13211 15125-15331 16116-16166 16244-16336 17085-17261 17834-18163 18315-19249 19368-20067 20077-20493 21715-21833
HFIAP91	121	925831	AC002094	2276	1-1458 1484-1825 2941-3033

					3149-3619 4464-4687
HFIAP91	121	925831	AC002094	2277	1-139 960-1288 3094-3333 3487-3622 4951-5037 5249-5369 5403-8947 9834-9970
HFIBI48	124	587871	AL162590	2278	1-574
HFIBI48	124	587871	AL161445	2279	1-574
HFIBI48	124	587871	AL162590	2280	1-697
HFIBI48	124	587871	AL162590	2281	1-326
HFIBI48	124	587871	AL161445	2282	1-326
HFIBI48	124	587871	AL161445	2283	1-697
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HOAAB15	213	575254	AC073970	2427	1-348
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HOAAH10	224	968368	AC009560	2469	1-606
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HOAAV23	230	527489	AC034291	2495	1-301
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HOABA93	234	792929	AC013335	2498	1-203
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HOABR40	238	531051	AC018603	2500	1-364
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HOEAY14	240	659258	AC074266	2506	1-352
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HFOYW76	905	769894	AL121926	3808	1-156 159-551
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HFOYV08	906	959038	Z98048	3810	1-2141 2561-2701 2941-3483 3789-4096 4140-5159 5304-6198 6305-6424 8034-8140 8775-9044 11025-11657 14599-15000 16088-16163 18758-18801 18856-19427 20301-20375

					23760-23837 24870-24955 25120-25391 26285-26348 27214-28161 28757-29091 31718-32125
HFOYV08	906	959038	Z98048	3811	1-507
HFOYN65	908	747740	AL358152	3812	1-1355 1765-2516
HFOYN65	908	747740	AL358152	3813	1-984
HFOYN65	908	747740	AL358152	3814	1-293
HFOYN01	909	854780	AC027228	3815	1-454 469-1300 1311-1530 3141-3500 3595-4461 5573-5640 6780-6854 6924-7105
HFOYN01	909	854780	AC027228	3816	1-538
HFOYM48	910	721455	AC000076	3817	1-615
HFOYM48	910	721455	AC000076	3818	1-1684
HFOYM48	910	721455	AC000076	3819	1-38 63-269 319-413 415-847 2369-3063 3084-5496
HFOYK21	912	670653	AC010895	3820	1-1048
HFOYK21	912	670653	AC010895	3821	1-381
HFOYH01	915	916055	AC008397	3822	1-1320
HFOYH01	915	916055	AC008397	3823	1-658 739-3456
HFOYA17	919	662642	AC008602	3824	1-348
HFOYA17	919	662642	AC008602	3825	1-113
HFOXW67	920	494854	AC024606	3826	1-1234
HFOXW67	920	494854	AC024606	3827	1-508
HFOXV94	921	794175	AC005328	3828	1-191 282-1004
HFOXV94	921	794175	AC005328	3829	1-347
HFOXV94	921	794175	AC005328	3830	1-913
HFOXT35	923	707088	AL354890	3831	1-527
HFOXT35	923	707088	AL354890	3832	1-270
HFOXs42	924	713514	AC015559	3833	1-739
HFOXs42	924	713514	AC015559	3834	1-831

HFOXO57	925	928171	AL022165	3835	1-4237
HFOXO57	925	928171	AL022165	3836	1-601
HFOXO57	925	928171	AL022165	3837	1-229
HFOXM53	927	587972	AC011314	3838	1-563
HFOXM53	927	587972	AC010742	3839	1-563 692-1031
HFOXM53	927	587972	AC011314	3840	1-247
HFOXM53	927	587972	AC010742	3841	1-247
HFOXM53	927	587972	AC010742	3842	1-307
HFOXK96	929	732057	AC004918	3843	1-70 582-1137 2262-2357 2561-7148 7282-10885
HFOXK96	929	732057	AC004918	3844	1-269
HFOXK96	929	732057	AC004918	3845	1-2013
HFOXK42	930	587960	AC006487	3846	1-385 925-963 1241-1694 1773-1934 2006-2474
HFOXK42	930	587960	AC006487	3847	1-1810
HFOXK42	930	587960	AC006487	3848	1-406
HFOXF91	931	790103	AC027731	3849	1-1854 2517-2610 2974-3261 3694-5322
HFOXF91	931	790103	AL355880	3850	1-1856 2517-2610 2974-3261 3694-5322 9187-9303 9508-9667 10248-10546 11270-11400 14251-14404 14486-14589 16590-16688 17066-17146
HFOXF91	931	790103	AL034379	3851	1-146 669-818 2394-2571 2805-3392 3477-3584 3993-4434 4623-4804 5144-5315

					7457-7544 7619-7747 8093-10079 10742-10835 11199-11486 11919-13547 17412-17528 17733-17892 18473-18771 19495-19625 22477-22630 24816-24914 25282-25405 25841-26405 26938-27002 29800-30272 30380-30568
HFOXF91	931	790103	AC027731	3852	1-129
HFOXF91	931	790103	AL355880	3853	1-110
HFOXF91	931	790103	AL034379	3854	1-392
HFOXD78	933	856499	AC010794	3855	1-3291
HFOXD78	933	856499	AC009985	3856	1-3291
HFOXD78	933	856499	AC010794	3857	1-92
HFOXD78	933	856499	AC010794	3858	1-4024 4342-4788 6234-6476 6856-7117 7574-7852
HFOXD78	933	856499	AC009985	3859	1-4023 4341-4787 6219-6532 6855-7116 7573-7851
HFOXB33	934	701719	AL049775	3860	1-633
HFOXB33	934	701719	AL049775	3861	1-734
HFIZP86	937	785341	AC013644	3862	1-1064
HFIZP86	937	785341	AC055747	3863	1-1617
HFIZP86	937	785341	AC013644	3864	1-611
HFIZP86	937	785341	AC055747	3865	1-147
HFIZP86	937	785341	AC055747	3866	1-611
HFIYX08	939	958977	AL158813	3867	1-446
HFIYX08	939	958977	AL096678	3868	1-446
HFIYX08	939	958977	AL158813	3869	1-233
HFIYX08	939	958977	AL158813	3870	1-528
HFIYX08	939	958977	AL096678	3871	1-233
HFIYX08	939	958977	AL096678	3872	1-528

HFIYW79	940	858618	AC025840	3873	1-240 265-775 2493-2540
HFIYW79	940	858618	AC008723	3874	1-798 1753-1907 2217-2531 3008-3156
HFIYW79	940	858618	AC008723	3875	1-951 1396-1557 5031-5131 7701-7878 8580-8685 8771-8930 8966-9330 9366-9665 13147-13262 16273-16490 17741-17892 18390-18570 18692-18768 20484-20585 20675-20764 20927-21397 22110-22308 22665-22845 24200-24245 25983-26076 26511-26819 27138-27218 27987-28086 30157-30255 30579-31026 31198-31314
HFIYS11	941	966702	AC058804	3876	1-491
HFIYS11	941	966702	AC058804	3877	1-508
HFIYN50	942	724175	AC026028	3878	1-577
HFIYN50	942	724175	AL353708	3879	1-456 936-1243 1296-2012
HFIYN50	942	724175	AL359853	3880	1-456 936-1243 1296-2012
HFIYN50	942	724175	AC026028	3881	1-423
HFIYN50	942	724175	AL359853	3882	1-2482 2605-3854
HFIYN50	942	724175	AL359853	3883	1-423
HFIYJ92	943	791305	AC000016	3884	1-65

					793-4089
HFIYJ92	943	791305	AC000016	3885	1-140
HFIXR93	947	894013	AL157824	3886	1-33 5109-7241 7282-11311
HFIXR93	947	894013	AC012151	3887	1-68 2079-2213 2879-2965 3114-3257 4198-4337 6080-6204 8566-8644 13691-19866
HFIXR68	948	752858	AC019198	3888	1-1725 2960-3425
HFIXR68	948	752858	AC015982	3889	1-1725 2960-3438 5180-5529 5615-5769 6070-6262 6580-7062
HFIXR68	948	752858	AC019198	3890	1-593
HFIXR68	948	752858	AC015982	3891	1-593
HFIXP31	949	697759	AC009761	3892	1-420 661-1011 1193-2688
HFIXP31	949	697759	AC009761	3893	1-369 518-912
HFIXP04	950	839910	AC009311	3894	1-564
HFIXP04	950	839910	AC009311	3895	1-319
HFIXP04	950	839910	AC009311	3896	1-183
HFIVS08	955	959272	AC007032	3897	1-163 511-831 1581-1856 1918-2584 2587-2776 3944-4761 4855-7799 7849-8034 8580-8847 9303-10448 11604-12183 12772-13476 13563-13793 14201-14557 14872-17303 17312-17604

					17739-18258 18373-19256 20321-20694 20846-22055 22122-22853 22866-23293 23557-24012 24021-24459 25225-28897
HFIVS08	955	959272	AC007032	3898	1-445
HFIVS08	955	959272	AC007032	3899	1-449
HFIUZ63	956	745033	AC016065	3900	1-1167 1243-2315 2390-2968
HFIUZ63	956	745033	AC018398	3901	1-1167 1243-2314 2389-2967
HFIUV58	958	735350	AC063952	3902	1-1120
HFIUV58	958	735350	AC063952	3903	1-1755
HFIUV18	959	787095	AC024064	3904	1-1333
HFIUV18	959	787095	AC024064	3905	1-161
HFIUM33	960	702319	AC073108	3906	1-595
HFIUM33	960	702319	AL161642	3907	1-562
HFIUM33	960	702319	AC004980	3908	1-457
HFIUM33	960	702319	AC073108	3909	1-113
HFIUM33	960	702319	AL161642	3910	1-101
HFIUM33	960	702319	AC073108	3911	1-101
HFIUM33	960	702319	AL161642	3912	1-1274 1766-2280 2300-2807 2837-3110
HFIUM33	960	702319	AC004980	3913	1-101
HFIUM33	960	702319	AC004980	3914	1-1274 1766-2280 2300-2807 2837-3110
HFIUH65	961	747836	AC022400	3915	1-1987
HFIUH65	961	747836	AC037447	3916	1-1922
HFIUH65	961	747836	AC022400	3917	1-621 646-1082 1155-1312
HFIUH65	961	747836	AC037447	3918	1-621 646-1082 1155-1312
HFIUD47	962	720254	AC018927	3919	1-1277
HFIUD47	962	720254	AC027797	3920	1-1277

HFIUD47	962	720254	AC018927	3921	1-518
HFIUD47	962	720254	AC027797	3922	1-517
HFITH46	963	718078	AC009220	3923	1-460 670-783 1321-1430 4578-4950 5053-5122 8113-8243 11039-11159 11712-11992 12016-12129 12648-12771
HFITH46	963	718078	AC009220	3924	1-122
HFIJF58	966	735927	AL049780	3925	1-860
HFIJF58	966	735927	AC006530	3926	1-860
HFIJF58	966	735927	AL049780	3927	1-1091
HFIJF58	966	735927	AL049780	3928	1-589
HFIJF58	966	735927	AC006530	3929	1-802
HFIJF58	966	735927	AC006530	3930	1-1090
HFIIR63	969	744994	AL354797	3931	1-693 700-1411
HFIIR63	969	744994	AC068485	3932	1-693 700-1411
HFIIR63	969	744994	AC013740	3933	1-4690 6959-7154 7209-7389 7431-7731 11120-11377 12689-12782 13980-14669 27508-27734 30606-31559 31691-32383 32390-33101 33665-33950 35646-35944 36682-36970 37681-38105 38961-39244 42417-42581 43432-43781 45418-45605 46318-46443 46498-46727
HFIIR63	969	744994	AL354797	3934	1-954
HFIIR63	969	744994	AL354797	3935	1-286
HFIIR63	969	744994	AC068485	3936	1-286

HFIIR63	969	744994	AC068485	3937	1-954
HFIIR63	969	744994	AC013740	3938	1-345 615-1006
HFIIR63	969	744994	AC013740	3939	1-231
HFIIRK75	971	767222	AC016722	3940	1-701 1766-2718
HFIIRK75	971	767222	AC016722	3941	1-717
HFIIRK07	973	953034	AC016394	3942	1-588 595-1084 1098-1581
HFIIRK07	973	953034	AC068557	3943	1-588 595-1083 1097-1580
HFIIRK07	973	953034	AC016394	3944	1-558 652-915 1677-5669 5844-5990 6502-6754 7996-8461 8748-8832 9129-9877
HFIIRK07	973	953034	AC068557	3945	1-558 652-915 1677-5156
HFIIRJ14	974	839523	AP001973	3946	1-102
HFIIRJ14	974	839523	AL355880	3947	1-34
HFIIRW16	976	858594	AC025891	3948	1-2095
HFIIRW16	976	858594	AC016173	3949	1-2712
HFIIRW16	976	858594	AP001600	3950	1-2711
HFIIRW16	976	858594	AC016173	3951	1-509
HFIIRW16	976	858594	AC016173	3952	1-463
HFIIRW16	976	858594	AP001600	3953	1-509
HFIIRW16	976	858594	AP001600	3954	1-187 869-1287 2982-3157 3423-3674 8406-8868
HFIIRW11	977	947856	AF254981	3955	1-57 1142-1260
HFIIRW11	977	947856	AC023188	3956	1-85 326-439 1924-2100 3184-3563
HFIIRW11	977	947856	AC023188	3957	1-204 939-1163
HFIIRW11	977	947856	AC023188	3958	1-475

HFIHV56	978	470954	AC022930	3959	1-121 959-1377 2087-2219 3018-3826 3852-4165 4657-4767 5284-5392 5999-6311 6327-6368 6940-7299 7610-8439
HFIHV56	978	470954	AF238376	3960	1-623 721-864 1041-1249 1439-1558 2395-2813 3523-3655 4454-5262 5288-5601 6093-6203 6720-6828 7435-7747 7763-7804 8376-8481 9046-9875
HFIHV56	978	470954	AF238376	3961	1-147 342-408
HFIHU76	979	769948	AC006995	3962	1-509
HFIHU76	979	769948	AC005098	3963	1-509
HFIHU76	979	769948	AC004166	3964	1-509
HFIHU76	979	769948	AC004883	3965	1-509
HFIHU76	979	769948	AC006995	3966	1-89
HFIHU76	979	769948	AC006995	3967	1-159
HFIHU76	979	769948	AC005098	3968	1-114 553-988 1601-1926 2188-2470 3568-3753 4168-4600 5038-5080 5881-5976 6271-6358 7128-8058 8786-10907
HFIHU76	979	769948	AC005098	3969	1-160
HFIHU76	979	769948	AC004166	3970	1-77 541-951

					1564-1889 2151-2235 3531-3716 4131-4563 4702-4802 5001-5043 5844-5939 6234-6321 7115-7476 7548-8020 8745-10867
HFIHU76	979	769948	AC004166	3971	1-163
HFIHU76	979	769948	AC004883	3972	1-114 459-988 1151-1251 1601-1926 2188-2470 3568-3753 4168-4600 5038-5080 5881-5976 6271-6358 7585-7796 7819-9872 10597-12718
HFIHU76	979	769948	AC004883	3973	1-163
HFIHS86	980	785419	AL158814	3974	1-1188
HFIHS86	980	785419	AL035694	3975	1-3503
HFIHS86	980	785419	AL035694	3976	1-131 3726-4036 9191-9552 10640-12003
HFIHK29	983	855174	AC012040	3977	1-1468
HFIHK29	983	855174	AC026464	3978	1-146 2144-2248 3425-4485 4538-6005 8727-8898 9137-9222 12214-12317 12384-12622 12696-12797 13071-13110 13572-15071
HFIHK29	983	855174	AC026474	3979	1-146 2144-2248 3425-4485

					4538-6005 9143-9228 12383-12621 12695-12796 13070-13109 13571-15070
HFIHK29	983	855174	AC026464	3980	1-568
HFIHK29	983	855174	AC012040	3981	1-146 2144-2248 3425-4485
HFIHK29	983	855174	AC026474	3982	1-568
HFIAL66	991	587837	AC012306	3983	1-565
HCDEL02	993	920831	AC061980	3984	1-628
HCDEL02	993	920831	AL159167	3985	1-1093 1477-1978
HCDEL02	993	920831	AC061980	3986	1-410
HCDEL02	993	920831	AL159167	3987	1-410
HCDEL02	993	920831	AL159167	3988	1-389
HCDDZ69	994	522220	AC002310	3989	1-256 411-537 2216-2825 2858-3950 4039-4108 4429-4979 5008-5410 5591-5625 5641-7301 7793-8106 8114-8234 11769-12452
HCDDZ69	994	522220	AC002310	3990	1-329
HCDDZ69	994	522220	AC002310	3991	1-1402 1469-3065
HCDDY54	995	529265	AC012488	3992	1-341
HCDDY54	995	529265	AC012488	3993	1-361
HCDDO80	996	778563	AC025165	3994	1-746
HCDDO80	996	778563	AC025165	3995	1-302
HCDCD64	997	863415	AC022197	3996	1-190
HCDCD64	997	863415	AC022197	3997	1-619
HCDBW41	998	712648	AP001325	3998	1-390
HCDBO86	999	784617	AC073487	3999	1-375 893-4326 4474-5168 5186-6317 6538-6708 6755-7192 7587-9453

HCDBO86	999	784617	AC023055	4000	1-246 485-1179 1198-2329 2550-2720 2767-3204 3603-5469
HCDBO86	999	784617	AC073487	4001	1-646
HCDBO86	999	784617	AC023055	4002	1-428
HCDBO86	999	784617	AC023055	4003	1-245
HCDAA68	1001	753814	AL353776	4004	1-560
HCDAA68	1001	753814	AL353776	4005	1-455
HCDAA68	1001	753814	AL353776	4006	1-130
HBACKF23	1003	675613	AC055747	4007	1-533 1236-1544 1697-1786
HBCGD25	1004	677689	AC023947	4008	1-691
HBCGD25	1004	677689	AC016946	4009	1-691
HBCGD25	1004	677689	AC022664	4010	1-691
HBCGD25	1004	677689	AC023947	4011	1-423
HBCGD25	1004	677689	AC016946	4012	1-423
HBCGD25	1004	677689	AC022664	4013	1-423
HBCGD25	1004	677689	AC016946	4014	1-100
HAOAE95	1005	795674	AC025225	4015	1-469 511-892 1010-2004
HAOAE95	1005	795674	AL034417	4016	1-469 511-892 1010-2004
HAOAE95	1005	795674	AC025225	4017	1-696
HAOAE95	1005	795674	AC025225	4018	1-430
HAOAE95	1005	795674	AL034417	4019	1-696
HAOAE95	1005	795674	AL034417	4020	1-430
HAOAD27	1006	848729	AL096776	4021	1-114 1783-2276 4713-5206 7371-10780
HAOAD27	1006	848729	AL096776	4022	1-418
HANKG10	1007	963926	AL353705	4023	1-565
HANKG10	1007	963926	AL353594	4024	1-565
HANKG10	1007	963926	AL353705	4025	1-405
HANKG10	1007	963926	AL353594	4026	1-405
HANKB13	1008	827062	AC023963	4027	1-139 1779-1929 2453-2599
HANKB13	1008	827062	AC023963	4028	1-610
HANKB13	1008	827062	AC023963	4029	1-349

HAMAC79	1009	872774	AC019066	4030	1-1701
HAMAC79	1009	872774	AC019066	4031	1-203

[066] Table 1B summarizes additional polynucleotides encompassed by the invention (including cDNA clones related to the sequences (Clone ID NO:Z), contig sequences (contig identifier (Contig ID:) contig nucleotide sequence identifiers (SEQ ID NO:X)), and genomic sequences (SEQ ID NO:B). The first column provides a unique clone identifier, "Clone ID NO:Z", for a cDNA clone related to each contig sequence. The second column provides the sequence identifier, "SEQ ID NO:X", for each contig sequence. The third column provides a unique contig identifier, "Contig ID:" for each contig sequence. The fourth column, provides a BAC identifier "BAC ID NO:A" for the BAC clone referenced in the corresponding row of the table. The fifth column provides the nucleotide sequence identifier, "SEQ ID NO:B" for a fragment of the BAC clone identified in column four of the corresponding row of the table. The sixth column, "Exon From-To", provides the location (i.e., nucleotide position numbers) within the polynucleotide sequence of SEQ ID NO:B which delineate certain polynucleotides of the invention that are also exemplary members of polynucleotide sequences that encode polypeptides of the invention (e.g., polypeptides containing amino acid sequences encoded by the polynucleotide sequences delineated in column six, and fragments and variants thereof).

TABLE 2

Clone ID NO:Z	Contig ID:	SEQ ID NO:X	Analysis Method	PFam/NR Description	PFam/NR Accession Number	Score/ Percent Identity	NT From	NT To
HANGC59	653577	20	HMMER 1.8	PFAM: Core histones H2A, H2B, H3 and H4	PF00125	11.44	96	164
HAOAE53	964029	41	HMMER 1.8	PFAM: Zinc finger, CCHC class	PF00098	6.5	136	168
HAOAE56	767915	42	blastx.2	(AF098066) squamous cell carcinoma antigen recognized by T cell [Homo sapiens]	gb AAF00087.1 AF 098066_1	88%	1	228
HBCKE78	746109	55	blastx.2	(AF038606) contains similarity to cytoskeletal keratin [Caenorhabditis elegans]	gb AAB92026.1	43%	55	225
HBFMC73	764150	56	blastx.2	(AK000496) unnamed protein product [Homo sapiens]	dbj BAA91205.1	66% 100%	210 23	22 3
HBSAL69	573004	58	blastx.2	23 kD protein [Escherichia coli]	gb AAA61994.1	71% 100% 60%	423 103 422	130 2 366
HBSAL80	506580	59	blastx.2	No definition line found [Escherichia coli]	gb AAB18589.1	86%	378	82
HBSAM48	727635	61	blastx.2	Pyruvate formate-lyase 1 activating enzyme (EC 1.97.1.4). [Escherichia coli]	dbj BAA35637.1	87%	56	322
HBSAP73	764589	63	blastx.2	homoserine kinase [Escherichia coli]	gb AAA20618.1	99%	467	3

HBSDDB50	571365	65	HMMER 2.1.1	PFAM: TCP-1/cpn60 chaperonin family	PF00118	89.7	2	226
			blastx.2	groEL protein (AA 1-548) [Escherichia coli]	emb CAA30698.1	79%	2	301
HBSDDB63	745211	66	blastx.2	(AF090895) PRO0117 [Homo sapiens]	gb AAF24019.1 AF 090895 1	68% 71%	224 91	93 71
HCDAE77	533925	70	blastx.2	(AC006539) BC39498_2 [Homo sapiens]	gb AAD14470.1	48% 46% 45% 48% 47% 40% 45% 42% 39% 35% 37% 35% 40% 63% 37%	59 59 59 62 62 59 59 62 59 11 7 4 4 4 241	238 232 238 223 238 238 238 238 217 238 69 69 69 36 309
HFICA06	934675	125	blastx.14	NADH:ubiquinone oxidoreductase MLRQ subunit [Homo sapiens]	gi 1946692 gb AAB 52726.1	82% 33% 66%	122 2 302	172 127 355
HFIE47	857988	140	blastx.2	weak similarity to ATP synthase B chain [Caenorhabditis elegans]	gb AAA50619.1	27% 37%	733 403	1644 687
HFIEF63	944246	141	HMMER 2.1.1	PFAM: Immunoglobulin domain	PF00047	22.4	92	364

HFITZ24	677144	152	HMMER 1.8	PFAM: Zinc finger, C2H2 type	PF00096	4.13	55	99
HFYTL01	919416	180	blastx.14	NADH:ubiquinone oxidoreductase MLRQ subunit [Homo sapiens]	gi 1946692 gb AAB52726.1	71% 38%	173 53	277 178
HMUBM26	908912	210	HMMER 2.1.1 blastx.2	PFAM: Zinc finger, C2H2 type zinc finger protein C2H2-25 [Homo sapiens]	PF00096 gb AAA93261.1	119.7 61% 62% 60% 60% 59% 59% 61% 50% 51% 40% 28% 83% 72% 72% 66% 64% 61% 68% 68% 63% 63% 50%	269 2 2 8 8 8 8 29 167 251 254 511 511 511 511 511 511 456 456 456 511	337 508 460 460 460 460 460 436 460 460 460 478 564 564 564 564 561 564 558 512 512 512 564

HOEAK21	954961	239	blastx.14	similar to Azorhizobium caulinodans hypoth. protein, 1	gi 396396 gb AAC4 3155.1	61%	511	564
HOEJG04	859251	261	HMMER 2.1.1	PFAM: Pyruvate flavodoxin/ferredoxin oxidoreductase (N terminus)	PF01855	227.6	3	431
HOEMK02	918364	267	blastx.14	Periplasmic chaperone focC protein [Escherichia coli]	gi 4062507 dbj BA A35694.1	100%	79	2
HOEOE25	907806	269	HMMER 1.8	PFAM: Zinc finger, C3HC4 type (RING finger)	PF00097	41.99	59	208
			blastx.2	(AJ224819) tumor suppressor [Homo sapiens]	emb CAA12136.1	41%	32	625
HRDAF69	956269	331	blastx.14	(AB012223) ORF2 [Canis familiaris]	gi 2981631 dbj BA A25253.1	42%	4	171
HRDBM42	530849	349	HMMER 1.8	PFAM: Helix-loop-helix DNA-binding domain	PF00010	8.1	139	246
HRDBT72	507847	356	HMMER 1.8	PFAM: Zinc-binding	PF00099	7.31	295	324

HSKET11	967000	441	blastx.14	metallopeptidase domain alternate name ygiP; ORF_310 [Escherichia coli]	gi 1203799 gb AAA89140.1	96% 100%	2 331	343 363
HSKHS71	911592	443	HMMER 2.1.1 blastx.14	PFAM: Ank repeat contains 10 ankyrin-like repeats; similar to human 1 [Paramecium bursaria Chlorella virus 1]	PF00023 gi 2447128 gb AAC96986.1	63.1 42% 36% 35% 35% 38% 31% 40% 35%	94 106 97 103 100 103 103 196 1	192 366 357 372 372 357 366 381 84
HSKKD70	916984	446	blastx.14	ORF_f268a [Escherichia coli]	gi 537144 gb AAA97199.1	93%	420	1
HSLBZ91	573987	467	HMMER 2.1.1	PFAM: Domain of unknown function	PF00990	78.1	6	254
HSLCJ47	908627	470	blastx.14	basoonuclin [Homo sapiens]	gi 179337 gb AAA35584.1	54%	263	361
HSLCL38	951028	471	blastx.14	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II [Escherichia coli]	gi 4062664 dbj BA A35903.1	88% 100%	41 3	202 41
HSLDG13	913664	477	blastx.14	melibiose carrier [Escherichia coli]	gi 146804 gb AAA24148.1	96% 66%	274 314	2 270
HSLDP16	573210	484	HMMER 2.1.1	PFAM: 6,7-dimethyl-8-ribitylumazine synthase	PF00885	184.6	8	271

HSLEC25	572859	487	HMMER 2.1.1	PFAM: Methylmalonyl-CoA mutase	PF01642	20	8	76
HSLED38	709381	489	HMMER 2.1.1	PFAM: Fructose-1-6-bisphosphatase	PF00316	47.3	369	473
HSLEG74	825500	493	HMMER 1.8	PFAM: Bacterial mutT protein	PF00293	2.42	30	98
HSLFS42	948740	501	blastx.14	RhsE protein (fragment). [Escherichia coli]	gi 1742368 dbj BA A15087.1	100% 100%	34 2	300 34
HSLFU01	916448	505	blastx.14	Rod protein FlgC [Escherichia coli]	gi 4062651 dbj BA A35882.1	89% 100% 100%	259 383 408	5 261 385
HSLIJ57	659533	517	HMMER 2.1.1	PFAM: Pyridoxal-dependent decarboxylase	PF00278	94	150	365
HSLJN49	920062	523	blastx.14	Spermidine/putrescine transport system permease protein PotB. [Escherichia coli]	gi 1651552 dbj BA A35945.1	98% 80%	246 427	1 245
HSSAN96	936108	567	blastx.14	(AF000531) Tat protein [Human immunodeficiency virus type 1]	gi 2245487 gb AAB 62530.1	63% 63% 30%	246 56 108	214 24 49
HSSBO48	871217	571	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	9.8	26	232
HSSEU93	911261	583	blastx.14	(AJ007012) Fish protein [Mus musculus]	gi 3702174 emb CA A07416.1	65% 39% 53% 54%	66 69 191 208	212 212 229 240

HSSAA15	965347	664	blastx.14	SM-20 [Rattus norvegicus]	gi 469478 gb AAA19321.1	77%	111	434
HSRAA80	937640	683	HMMER 1.8	PFAM: Reverse transcriptase (RNA-dependent DNA polymerase)	PF00078	20.88	11	130
			blastx.14	(AF080232) polymerase [Human endogenous retrovirus K]	gi 3600069 gb AAC63292.1	65%	17	325
HSLKB62	905738	690	HMMER 2.1.1	PFAM: Transglycosylase	PF00912	310.2	344	850
			blastx.14	ORF_f242 [Escherichia coli]	gi 606147 gb AAA58010.1	93%	290	937
HSLJF33	938811	694	blastx.2	(AE000391) putative transport protein [Escherichia coli]	gb AAC76123.1	84%	3	527
HSLJD02	965826	695	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	19.53	464	874
			blastx.2	UhpC protein [Escherichia coli]	gb AAA24722.1	100%	56	907
HSLHZ10	963808	701	blastx.14	Hypothetical 17.3 kd protein in alpA-gabD intergenic region (o152). [Escherichia coli]	gi 4902983 dbj BA A77917.1	97% 100%	308 178	180 128
HSLHV27	964075	702	HMMER 2.1.1	PFAM: NADH-Ubiquinone/plastoquinone (complex I), various chains	PF00361	115.1	917	615

HSLGO19	668634	708	blastx.2	NADH dehydrogenase I, subunit nuoL [Escherichia coli]	emb CAA48371.1	99%	91	954
			HMMER 1.8	PFAM: Basic region plus leucine zipper transcription factors	PF00170	17.19	265	372
HSLGA24	955333	722	HMMER 2.1.1	PFAM: Mur ligase family	PF01225	119.9	772	386
			blastx.2	UDP-MurNac-tripeptide synthetase (MurE) [Escherichia coli]	dbj BAA01350.1	91% 99%	33 434	476 805
HSLFT29	680451	724	HMMER 1.8	PFAM: Sigma-70 factors	PF00140	224.55	1	399
HSLDT25	949079	730	HMMER 2.1.1	PFAM: FecCD transport family	PF01032	86.6	1331	921
			blastx.2	ferrichrome-iron transport protein FhuB [Escherichia coli]	gb AAB08583.1	92% 97% 35% 28% 69%	32 661 673 101 3	712 1026 1011 613 41
HSLDR05	932128	732	blastx.14	UhpC protein [Escherichia coli]	gi 148114 gb AAA24722.1	97% 100% 42%	98 3 127	220 95 168
HSLCX61	742031	738	HMMER 2.1.1	PFAM: KRAB box	PF01352	49.2	373	474
HSLCF96	637670	739	HMMER 1.8	PFAM: Sugar (and other) transporters	PF00083	10.78	415	576
			blastx.2	(AE000352) putative	gb AAC75728.1	94%	415	1179

HSKCF96	954777	1016	HMMER 1.8	transport protein [Escherichia coli]		100%	297	413
						70%	1101	1211
						20%	409	600
						26%	1021	1179
						30.03	1296	1015
						96%	303	1127
						91%	1147	1215
HSKKE11	965857	744	blastx.14	cDNA EST EMBL:D70203 comes from this gene; cDNA EST 1 1 yk403g7.5 comes from this gene; cDNA EST EMBL:C08962 comes from	g 3877299 emb CA A93496.1	88%	117	245
						62%	28	75
						100%	3	26
HSKHT93	957866	749	blastx.14	(AF117815) molybdopterin synthase small subunit [Homo sapiens]	g 4235630 gb AAD 13296.1	80%	275	364
HSKEH21	941976	752	blastx.14	diacylglycerol kinase eta [Cricetinae gen. sp.]	g 1401232 gb AAC 52714.1	87%	8	703
HSKCR54	922730	754	HMMER 2.1.1	PFAM: Ribosomal protein L17	PF01196	29.6	260	394
HSKBW86	785783	756	HMMER 2.1.1	PFAM: Bacterial surface antigen	PF01103	75.2	1	165
HSKCL04	840406	765	blastx.2	(AF118082) PRO1902 [Homo sapiens]	gb AAF22026.1 AF 118094 21	70%	651	559
						61%	326	273

HOSMP95	948496	794	blastx.14	unknown [Mus musculus]	gi 1490330 emb CA B01546.1	77%	3	146
HOSCV06	960555	809	blastx.2	(AL133104) hypothetical protein [Homo sapiens]	emb CAB61411.1	100%	45	191
HOHAV60	489007	842	HMMER 1.8	PFAM: PH (pleckstrin homology) domain	PF00169	15.98	111	212
HOHAI11	965035	1026	blastx.14	10-formyltetrahydrofolate dehydrogenase [Rattus norvegicus]	gi 908915 gb AAA70429.1	69% 100%	102 431	422 448
HOEEU57	932562	853	HMMER 2.1.1	PFAM: MYND finger	PF01753	45.6	139	255
HOABG91	811156	863	blastx.14	skm-BOP2 [Mus musculus]	gi 5870834 gb AAC53022.2	39%	76	279
						41%	556	750
						22%	289	552
HOABG91	811156	863	HMMER 1.8	PFAM: Low-density lipoprotein receptor domain class B	PF00058	23.5	46	174
HFOZC29	923288	903	blastx.14	coatamer [Bos taurus]	gi 441486 emb CA A53539.1	87%	568	422
HFOYG86	955554	1029	blastx.2	G protein-coupled receptor [Lymnaea stagnalis]	emb CAA80651.1	31%	8	727
HFOXL88	909839	928	blastx.14	(AC004084) similar to GTPase-activating proteins; 1	gi 2822157 gb AAB97935.1	97%	305	171
						100%	425	303
						72%	180	148
						83%	411	394

HFIXP31	697759	949	HMMER 2.1.1	PFAM: BTB/POZ domain	PF00651	49.8	9	146
HFTHW91	907618	975	HMMER 2.1.1	PFAM: ADP- ribosylation factor family	PF00025	82.4	222	500
			blastx.14	GTP-binding protein [Drosophila melanogaster]	gi 290213 gb AAA7 4629.1	31% 54%	288 222	488 287
HFTHW11	947856	977	blastx.14	Similarity to Yeast TAT-binding homolog 7 1 1 1 EMB	gi 4008355 emb CA A92596.1	81%	3	146
HFIDL68	928475	986	HMMER 1.8	PFAM: 7 transmembrane receptor (rhodopsin family)	PF00001	50.42	8	319
			blastx.2	G protein-coupled receptor [Lymnaea stagnalis]	emb CAA80651.1	41%	11	340
HFIBK83	939556	988	blastx.14	contains similarity to ATP/GTP-binding site motif (PS:PS00017) [Caenorhabditis elegans]	gi 1519671 gb AAB 07572.1	38%	20	289
HCOKA10	907080	992	HMMER 2.1.1	PFAM: Ribosomal protein L34e	PF01199	229.8	509	213
			blastx.2	ribosomal protein L34 [Homo sapiens]	gb AAC41916.1	98%	521	216
HCOKA10	918918	1031	HMMER 2.1.1	PFAM: Small cytokines (interleukin-8 like)	PF00048	124.2	1447	1238

			blastx.14	granulocyte chemotactic protein, GCP-2 - bovine	pir B54188 B54188	100%	1444	1223
HCOKA10	919869	1032	HMMER 2.1.1	PFAM: Small cytokines (intecrine/chemokine), interleukin-8 like	PF00048	124.2	169	378

[067] Table 2 further characterizes certain encoded polypeptides of the invention, by providing the results of comparisons to protein and protein family databases. The first column provides a unique clone identifier, "Clone ID NO:", corresponding to a cDNA clone disclosed in Table 1A. The second column provides the unique contig identifier, "Contig ID:" which allows correlation with the information in Table 1A. The third column provides the sequence identifier, "SEQ ID NO:X", for the contig polynucleotide sequences. The fourth column provides the analysis method by which the homology/identity disclosed in the row was determined. The fifth column provides a description of PFam/NR hits having significant matches identified by each analysis. Column six provides the accession number of the PFam/NR hit disclosed in the fifth column. Column seven, "Score/Percent Identity", provides a quality score or the percent identity, of the hit disclosed in column five. Comparisons were made between polypeptides encoded by polynucleotides of the invention and a non-redundant protein database (herein referred to as "NR"), or a database of protein families (herein referred to as "PFam"), as described below.

[068] The NR database, which comprises the NBRF PIR database, the NCBI GenPept database, and the SIB SwissProt and TrEMBL databases, was made non-redundant using the computer program nrdb2 (Warren Gish, Washington University in Saint Louis). Each of the polynucleotides shown in Table 1A, column 3 (e.g., SEQ ID NO:X or the 'Query' sequence) was used to search against the NR database. The computer program BLASTX was used to compare a 6-frame translation of the Query sequence to the NR database (for information about the BLASTX algorithm please see Altshul et al., J. Mol. Biol. 215:403-410 (1990), and Gish et al., Nat. Genet. 3:266-272 (1993)). A description of the sequence that is most similar to the Query sequence (the highest scoring 'Subject') is shown in column five of Table 2 and the database accession number for that sequence is provided in column six. The highest scoring 'Subject' is reported in Table 2 if (a) the estimated probability that the match occurred by chance alone is less than $1.0e-07$, and (b) the match was not to a known repetitive element. BLASTX returns alignments of short polypeptide segments of the Query and Subject sequences which share a high degree of similarity; these segments are known as High-Scoring Segment Pairs or HSPs. Table 2 reports the degree of similarity between the Query and the Subject for each HSP as a percent identity in Column 7.

The percent identity is determined by dividing the number of exact matches between the two aligned sequences in the HSP, dividing by the number of Query amino acids in the HSP and multiplying by 100. The polynucleotides of SEQ ID NO:X which encode the polypeptide sequence that generates an HSP are delineated by columns 8 and 9 of Table 2.

[069] The PFam database, PFam version 5.2, (Sonnhammer et al., Nucl. Acids Res., 26:320-322, (1998)) consists of a series of multiple sequence alignments; one alignment for each protein family. Each multiple sequence alignment is converted into a probability model called a Hidden Markov Model, or HMM, that represents the position-specific variation among the sequences that make up the multiple sequence alignment (see, e.g., R. Durbin et al., *Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998 for the theory of HMMs). The program HMMER version 1.8 (Sean Eddy, Washington University in Saint Louis) was used to compare the predicted protein sequence for each Query sequence (SEQ ID NO:Y in Table 1A) to each of the HMMs derived from PFam version 5.2. A HMM derived from PFam version 5.2 was said to be a significant match to a polypeptide of the invention if the score returned by HMMER 1.8 was greater than 0.8 times the HMMER 1.8 score obtained with the most distantly related known member of that protein family. The description of the PFam family which shares a significant match with a polypeptide of the invention is listed in column 5 of Table 2, and the database accession number of the PFam hit is provided in column 6. Column 7 provides the score returned by HMMER version 1.8 for the alignment. Columns 8 and 9 delineate the polynucleotides of SEQ ID NO:X which encode the polypeptide sequence which shows a significant match to a PFam protein family.

[070] As mentioned, columns 8 and 9 in Table 2, "NT From" and "NT To", delineate the polynucleotides of "SEQ ID NO:X" that encode a polypeptide having a significant match to the PFam/NR database as disclosed in the fifth column of Table 2. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the polynucleotides of SEQ ID NO:X delineated in columns 8 and 9 of Table 2. Also provided are polynucleotides encoding such proteins, and the complementary strand thereto.

[071] The nucleotide sequence SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, the nucleotide sequences of SEQ ID NO:X are useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in Clone ID NO:Z. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to these polypeptides, or fragments thereof, and/or to the polypeptides encoded by the cDNA clones identified in, for example, Table 1A.

[072] Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

[073] Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, and a predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing cDNA Clone ID NO:Z deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

[074] The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

RACE Protocol For Recovery of Full-Length Genes

[075] Partial cDNA clones can be made full-length by utilizing the rapid amplification of cDNA ends (RACE) procedure described in Frohman, M.A., et al., Proc. Nat'l. Acad. Sci. USA, 85:8998-9002 (1988). A cDNA clone missing either the 5' or 3' end can be reconstructed to include the absent base pairs extending to the translational start or stop codon, respectively. In some cases, cDNAs are missing the start codon of translation. The following briefly describes a modification of this original 5' RACE procedure. Poly A⁺ or total RNA is reverse transcribed with Superscript II (Gibco/BRL) and an antisense or complementary primer specific to the cDNA sequence. The primer is removed from the reaction with a Microcon Concentrator (Amicon). The first-strand cDNA is then tailed with dATP and terminal deoxynucleotide transferase (Gibco/BRL). Thus, an anchor sequence is produced which is needed for PCR amplification. The second strand is synthesized from the dA-tail in PCR buffer, Taq DNA polymerase (Perkin-Elmer Cetus), an oligo-dT primer containing three adjacent restriction sites (XhoI, SalI and ClaI) at the 5' end and a primer containing just these restriction sites. This double-stranded cDNA is PCR amplified for 40 cycles with the same primers as well as a nested cDNA-specific antisense primer. The PCR products are size-separated on an ethidium bromide-agarose gel and the region of gel containing cDNA products the predicted size of missing protein-coding DNA is removed. cDNA is purified from the agarose with the Magic PCR Prep kit (Promega), restriction digested with XhoI or SalI, and ligated to a plasmid such as pBluescript SKII (Stratagene) at XhoI and EcoRV sites. This DNA is transformed into bacteria and the plasmid clones sequenced to identify the correct protein-coding inserts. Correct 5' ends are confirmed by comparing this sequence with the putatively identified homologue and overlap with the partial cDNA clone. Similar

methods known in the art and/or commercial kits are used to amplify and recover 3' ends.

[076] Several quality-controlled kits are commercially available for purchase. Similar reagents and methods to those above are supplied in kit form from Gibco/BRL for both 5' and 3' RACE for recovery of full length genes. A second kit is available from Clontech which is a modification of a related technique, SLIC (single-stranded ligation to single-stranded cDNA), developed by Dumas et al., *Nucleic Acids Res.*, 19:5227-32 (1991). The major differences in procedure are that the RNA is alkaline hydrolyzed after reverse transcription and RNA ligase is used to join a restriction site-containing anchor primer to the first-strand cDNA. This obviates the necessity for the dA-tailing reaction which results in a polyT stretch that is difficult to sequence past.

[077] An alternative to generating 5' or 3' cDNA from RNA is to use cDNA library double-stranded DNA. An asymmetric PCR-amplified antisense cDNA strand is synthesized with an antisense cDNA-specific primer and a plasmid-anchored primer. These primers are removed and a symmetric PCR reaction is performed with a nested cDNA-specific antisense primer and the plasmid-anchored primer.

RNA Ligase Protocol For Generating The 5' or 3' End Sequences To Obtain Full Length Genes

[078] Once a gene of interest is identified, several methods are available for the identification of the 5' or 3' portions of the gene which may not be present in the original cDNA plasmid. These methods include, but are not limited to, filter probing, clone enrichment using specific probes and protocols similar and identical to 5' and 3' RACE. While the full length gene may be present in the library and can be identified by probing, a useful method for generating the 5' or 3' end is to use the existing sequence information from the original cDNA to generate the missing information. A method similar to 5' RACE is available for generating the missing 5' end of a desired full-length gene. (This method was published by Fromont-Racine et al., *Nucleic Acids Res.*, 21(7):1683-1684 (1993)). Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcript. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest, is

used to PCR amplify the 5' portion of the desired full length gene which may then be sequenced and used to generate the full length gene. This method starts with total RNA isolated from the desired source, poly A RNA may be used but is not a prerequisite for this procedure. The RNA preparation may then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA, which may interfere with the later RNA ligase step. The phosphatase, if used, is then inactivated and the RNA is treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase. This modified RNA preparation can then be used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction can then be used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the musculoskeletal system antigen of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the relevant musculoskeletal system antigen.

[079] The present invention also relates to vectors or plasmids, which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC (deposited with the ATCC on October 5, 2000, and receiving ATCC designation numbers PTA 2574 and PTA 2575; deposited with the ATCC on January 5, 2001, having the depositor reference numbers TS-1, TS-2, AC-1, and AC-2; and/or as set forth, for example, in Table 1A, 6 and 7) is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown, for example, in Table 7. These deposits are referred to as "the deposits" herein. The tissues from which some of the clones were derived are listed in Table 7, and the vector in which the corresponding cDNA is contained is also indicated in Table 7. The deposited material includes cDNA clones corresponding to SEQ ID NO:X described, for example, in Table 1A (Clone ID NO:Z). A clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X, may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Furthermore,

although the sequence listing may in some instances list only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to sequence the DNA included in a clone contained in the ATCC Deposits by use of a sequence (or portion thereof) described in, for example Tables 1A or 2 by procedures hereinafter further described, and others apparent to those skilled in the art.

[080] Also provided in Table 7 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

[081] Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128,256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res.* 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res.* 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies* 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

[082] Vectors pSport1, pCMVSPORT 1.0, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus* 15:59- (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res.* 16:9677-9686 (1988) and Mead, D. et al., *Bio/Technology* 9: (1991).

- [083] The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the deposited clone (Clone ID NO:Z). The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.
- [084] Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of musculoskeletal system associated genes corresponding to SEQ ID NO:X or the complement thereof, polypeptides encoded by SEQ ID NO:X or the complement thereof, and/or the cDNA contained in Clone ID NO:Z, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.
- [085] The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.
- [086] The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.
- [087] The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides

of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the musculoskeletal system polypeptides of the present invention in methods which are well known in the art.

[088] The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA sequence contained in Clone ID NO:Z. The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X or a complement thereof, a polypeptide encoded by the cDNA contained in Clone ID NO:Z, and/or the polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, a polypeptide encoded by the cDNA contained in Clone ID NO:Z and/or a polypeptide sequence encoded by a nucleotide sequence in SEQ ID NO:B as defined in column 6 of Table 1B are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, a nucleic acid sequence encoding a polypeptide encoded by the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the cDNA contained in Clone ID NO:Z.

[089] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in Table 1B column 6, or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table

1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[090] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B,

column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[091] Further, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2), or any combination thereof. In further embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in column 6 of Table 1B which correspond to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (See Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides and polypeptides are also encompassed by the invention.

[092] Moreover, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. Additional, representative examples of polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, or any combination thereof. In preferred embodiments, the polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the complementary strand(s) of the sequences delineated in the same row of Table 1B column 6, wherein sequentially delineated sequences in the table (i.e. corresponding to those exons located closest to each other) are directly contiguous in a 5' to 3' orientation. In further embodiments, above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that of the BAC fragment having the sequence disclosed in SEQ ID NO:B (see Table 1B, column 5). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that published for the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). In additional embodiments, the above-described polynucleotides of the invention comprise, or alternatively consist of, sequences delineated in the same row of Table 1B, column 6, and have a nucleic acid sequence which is different from that contained in the BAC clone identified as BAC ID NO:A (see Table 1B, column 4). Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[093] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1B, column 2) or fragments or variants thereof. Polypeptides encoded by these polynucleotides, other

polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[094] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in column 6 of Table 1B which correspond to the same Clone ID NO:Z (see Table 1B, column 1), and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same Clone ID NO:Z. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[095] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, one, two, three, four, five, six, seven, eight, nine, ten, or more of the sequences delineated in the same row of column 6 of Table 1B, and the polynucleotide sequence of SEQ ID NO:X (e.g., as defined in Table 1A or 1B) or fragments or variants thereof. In preferred embodiments, the delineated sequence(s) and polynucleotide sequence of SEQ ID NO:X correspond to the same row of column 6 of Table 1B. Polypeptides encoded by these polynucleotides, other polynucleotides that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention.

[096] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of the sequence of SEQ ID NO:X are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids that encode these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[097] In additional specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X are directly contiguous Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[098] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[099] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of a fragment or variant of the sequence of SEQ ID NO:X and the 5' 10 polynucleotides of the sequence of one of the sequences delineated in column 6 of Table 1B are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other

polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides, are also encompassed by the invention.

[0100] In further specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0101] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same Clone ID NO:Z (see Table 1B, column 1) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0102] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of, a polynucleotide sequence in which the 3' 10 polynucleotides of one sequence in column 6 corresponding to the same contig sequence identifier SEQ ID NO:X (see Table 1B, column 2) are directly contiguous. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent

hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0103] In specific embodiments, polynucleotides of the invention comprise, or alternatively consist of a polynucleotide sequence in which the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B and the 5' 10 polynucleotides of another sequence in column 6 corresponding to the same row are directly contiguous. In preferred embodiments, the 3' 10 polynucleotides of one of the sequences delineated in column 6 of Table 1B is directly contiguous with the 5' 10 polynucleotides of the next sequential exon delineated in Table 1B, column 6. Nucleic acids which hybridize to the complement of these 20 contiguous polynucleotides under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention. Polypeptides encoded by these polynucleotides and/or nucleic acids, other polynucleotides and/or nucleic acids encoding these polypeptides, and antibodies that bind these polypeptides are also encompassed by the invention. Additionally, fragments and variants of the above-described polynucleotides, nucleic acids, and polypeptides are also encompassed by the invention.

[0104] Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. Accordingly, for each contig sequence (SEQ ID NO:X) listed in the third column of Table 1A, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 and the final nucleotide minus 15 of SEQ ID NO:X, b is an integer of 15 to the final nucleotide of SEQ ID NO:X, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:X, and where b is greater than or equal to a + 14. More specifically, preferably excluded are one or more polynucleotides

comprising a nucleotide sequence described by the general formula of a-b, where a and b are integers as defined in columns 4 and 5, respectively, of Table 3. In specific embodiments, the polynucleotides of the invention do not consist of at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. as disclosed in column 6 of Table 3 (including for example, published sequence in connection with a particular BAC clone). In further embodiments, preferably excluded from the invention are the specific polynucleotide sequence(s) contained in the clones corresponding to at least one, two, three, four, five, ten, or more of the available material having the accession numbers identified in the sixth column of this Table (including for example, the actual sequence contained in an identified BAC clone). In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example. All references available through these accessions are hereby incorporated by reference in their entirety.

TABLE 3

Clone ID NO: Z	SEQ ID NO: X	Contig ID:	EST Disclaimer Range of a Range of b	Accession #'s
HANGA63	11	927404	1 - 248	AL133312.
HANGA69	12	718174	1 - 431	
HANGA85	13	746265	1 - 305	
HANGA92	14	791182	1 - 134	
HANGC05	15	674059	1 - 144	
HANGC07	16	952586	1 - 212	
HANGC14	17	952581	1 - 246	
HANGC30	18	966430	1 - 324	
HANGC33	19	702072	1 - 237	
HANGC59	20	653577	1 - 167	AI128945, AA181985, AI051473, AI811806, AI742394, AI796471, AA047524, AW168284, AA644217, AA461312, AA223990, AI702471, AA449477, AI344611, AI084340, AA047404, AI982714, AI655453, AI609227, AI953345, AI918075, AI074844, AI948767, AI823646, AI125444, Z40657, AI942374, AA773940, AW303808, AA996094, AW235687, AI718217, AW081809, AW339488, R97621, AA678046, AA569360, AI581387, AI245396, T80973, AL121270, AI671642, AI499483, AL045163, AA809974, AW020592, AL039276, AA715307, AI863629, AI624543, AW189802, AA425228, AA975588, AL045620, AW084056, AI923509, AA748353, AI064830, AL121328, AA525540, AA768725, AI890507, AA761557, N72726, AI343091, AI364788, AW117882, AL119748, AI805774, F37323, AI289791, AL043152, AL045500, AI557808, AI432644, AI702065, AI273179, AW087445, AI494201, AA641818, AI624279, AI927233, AI312325, AL110402, AI269862, AW161202, AI307604, AW019988, AW020419, AI433157, AI648567, AI690946, AI554821, AW151136, N99180, AW081349, AA848069, AI539771, AI537677, AI636581, AW410430, AI500659, AI866465, AI815232, AI801325, AW082113, AL045413, AI500523, AI538850, AI431307, AI887775, AI582932, AI590043, AI872423, AI284517, AI923989, AI866786, AI500706, AI445237, AI491776, AW151138, AI521560, AI889189, AI500662, AW172723, AI582912, AI539800, AI284509, AI889168, AI440263, AI538885, AI866573, AI633493, AI434256, AI866469, AI805769, AI434242, AI888661, AW196105, AI500714, AI284513, AI888118, AI285439, AI859991, AI436429, AI355779, AI889147,

<p> AI623736, AI371228, AI581033, AI491710, AI440252, AI860003, AI610557, AW162194, AI242736, AW075382, AI828574, AI887499, AW151979, AI539781, AI539707, AW071377, AI866820, AI885949, AI785419, AW089557, AI559957, AI521571, AI469775, AI866581, AL048644, AI567953, AI815150, AI446495, AL042595, AL042745, AW023351, AA743430, AW162189, AL047422, H41759, AI348897, AI433037, AI633125, AL041150, AI475817, AI612750, AL037582, AL037602, AL043981, AI909696, AI345688, AA460184, R75918, AI867068, AL043168, AW197139, AI525669, AI431316, AI275175, AI890907, AA857847, AI307494, AW022494, AW269097, AW265004, AI499890, AL040243, AW268072, AW268261, AI345608, AI636372, AI620284, AA575874, AI567582, AW020288, AI879064, AI309443, AL038564, AI565172, AL039783, AW083804, AI345471, AW022299, AL042628, AI561170, AW191003, AI702527, AW020425, AL079799, N27632, AI336585, AW020710, AI921057, AI623941, AI309401, AL120254, AI923046, AL048375, F36003, AL042627, AI866510, AI557238, AI446373, AL039390, AL042365, AL038605, AW238730, AI866461, AF081195, AL117440, Z99297, AL122049, AF081197, AC004805, AP000030, E06743, AL137665, E01314, AL137574, AL117457, AF141289, AL117435, S68736, I48978, AF113019, S63521, S77771, AF111851, A03736, M92439, AC006203, AL133072, I89947, AC004213, AR038854, AF162270, Y10080, I46765, Z49258, U77594, A08913, AI8777, Z72491, AL122106, AC005874, AF134471, A08912, A08910, A08909, I89931, L30117, AL034376, AF026124, AF036268, AF158248, I49625, AL122110, AF113690, A08908, AL133080, AL133081, S76508, AL133077, AL133049, AR011880, AF110520, AF067728, AF058921, AL137558, I89934, I00734, Y10655, D83989, AR020905, AF100931, L19437, AL137478, AL137271, AF153205, AF094480, AL117649, A91160, E00617, E00717, E00778, AL050092, AL137548, X96540, X72889, AF113013, A08916, A65340, AL049314, AF125948, AF022813, AR053103, AL031732, AC004544, AF113689, Y10823, S36676, AL080110, AF111849, AF090886, AL122121, AC004686, AL033521, AF078844, Z13966, AF114818, AC008067, AL110221, M27260, AC005048, AJ010277, AL133568, U80742, I03321, AC004383, E07361, D55641, Y11587, AL050277, E02349, Y14314, A08907, X67813, U42766, AF061943, AL031274, Z82206, AC004594, AB007812, AF061795, AF151685, E06788, E06790, E06789, AJ012755, AL050310, AF169154, AF002985, Z98036, AC004989, S75997, AF003737, I89944, A07588, A65341, U67958, AL049382, AL133640, AL050172, Z82022, AF183393, AL137554, AF106697, I05032, AF113676, X06146, AF151109, AL137488, X93495, AL133565, </p>				
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HANGC84	21	715991	1 - 440	15 - 454		
HANGF36	22	952583	1 - 263	15 - 277		
HANGF49	23	722635	1 - 112	15 - 126		AC007320.
HANGG22	24	848727	1 - 347	15 - 361		
HANGH48	25	718759	1 - 410	15 - 424		
HANGH53	26	727914	1 - 460	15 - 474		
HANGH58	27	811987	1 - 393	15 - 407		
HANGH66	28	661513	1 - 442	15 - 456		
HANKD09	29	625167	1 - 334	15 - 348		
HANKD47	30	719963	1 - 425	15 - 439		
HANKD83	31	963964	1 - 300	15 - 314		
HANKG78	32	710760	1 - 180	15 - 194		
HANKG90	33	746282	1 - 410	15 - 424		
HANKH48	34	721340	1 - 343	15 - 357		
HANKH56	35	733063	1 - 360	15 - 374		
HAOAA57	36	955693	1 - 228	15 - 242		AW138563, W39428, AA441848, AI928563, AW138262, AI825038, AA985573, AW162121, AA063432, AA583586, AW341116, AA372242, N26196, H50245, AI565281, AA861973, AA338299, T85197, C00398, AI810565, and AF187318.
HAOAA78	37	756979	1 - 544	15 - 558		
HAOAA90	38	919249	1 - 321	15 - 335		
HAOAC05	39	932017	1 - 502	15 - 516		
HAOAD47	40	864899	1 - 473	15 - 487		AC005495.
HAOAE53	41	964029	1 - 368	15 - 382		
HAOAE56	42	767915	1 - 323	15 - 337		AI927761, AW378374, AI932972, AI690765, T58205, AF098066, and Z84488.
HAOAE60	43	657909	1 - 226	15 - 240		AA348977.
HAOAF68	44	752788	1 - 951	15 - 965		AA031836, AA031837, AA909082, and AL134312.
HAOAH38	45	705946	1 - 325	15 - 339		AC005036.
HAOMA1	46	915881	1 - 414	15 - 428		

HAOMB64	47	960293	1 - 599	15 - 613	
HAOMC21	48	670518	1 - 542	15 - 556	
HAOMD9 0	49	788658	1 - 395	15 - 409	AL050343.
HAOME45	50	705947	1 - 506	15 - 520	
HBCGA72	51	756953	1 - 137	15 - 151	AI126076, AI539265, AI458605, AW379387, and AW368357.
HBCKB24	52	676825	1 - 482	15 - 496	
HBCKB82	53	779562	1 - 522	15 - 536	AA961486.
HBCKE22	54	674041	1 - 147	15 - 161	AI954693, AI656728, AI281560, and AA491824.
HBCKE78	55	746109	1 - 647	15 - 661	AA204666, AA171635, AA632321, AA814237, AA631958, AW389228, AI167680, AI274831, AW023312, AA860756, AA631959, AW450236, T49450, AI168544, AI332870, AB014543, AC004494, and AC004224.
HBFCMC73	56	764150	1 - 385	15 - 399	AL135357, AW196064, AI002744, AA536040, AA515905, AA502860, AA493708, AI524360, AI252274, AI591375, AW274349, AA527602, AI053911, AI872020, AA658362, AA595499, AW020992, AA580808, AA630672, F17555, AA847499, AW237875, AI249880, AL046409, AA531079, AW302711, AA715814, AW270784, AI267269, AA613232, AI791913, AA527727, AI674873, AI792133, AI053560, AI821714, AI564185, AA574442, AI476049, AA664909, AA493845, AI687343, AA642060, AA297666, AA521323, AW339622, AW303196, AI144081, AA362698, AL037771, AA521399, AA621381, AA679532, AA749235, AI499938, AA652677, AA806796, AI744306, AI682665, AI821785, AW378968, AC007540, AP000495, AC004686, AC006151, AC005324, AC002352, AC005183, AC005859, AC004150, AL031311, AL117693, AF129756, AC004815, AC003982, AF196779, AC004019, Z97053, AC004383, AC004895, AL109829, AC005736, AL096867, AC006130, AC004144, AP000696, AL132796, AP000504, AC002115, AL021940, AC004263, Z68321, AC007617, AC004912, AC002395, D83989, AC007919, AC003006, U85195, AL021397, AC005799, AC002091, AE000658, AP000356, AC005327, AC005911, AC000052, AC007073, AL031597, Z93241, AL021155, AL022302, AC005863, AL031255, AC003109, AC004253, AP000044, AP000112, AC005668, AC002563, AC003689, AP000088, AP000365, AL110502, AC007649, AL080285, AL023575, AC004167, X75335, AL080114, Z99756, AC006985, AC006649, AC004821, AP000548, AC007114, AC004008, AL109628, AP000359, AC000353, AL008730, AL031003, AC006511, AC005822, AL030997, AP000117, AL034451, U89337, AC001231, AL035072, AC006251, AC002350, Z82976, AL035405, AC004655, AP000354, AL009177, AP000143, AC007371, AC006057, AC005261,

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HBSAK76	57	506666	1 - 265	15 - 279	
HBSAL69	58	573004	1 - 419	15 - 433	
HBSAL80	59	506580	1 - 366	15 - 380	
HBSAM46	60	526732	1 - 331	15 - 345	
HBSAM48	61	727635	1 - 393	15 - 407	
HBSAP02	62	920648	1 - 325	15 - 339	
HBSAP73	63	764589	1 - 454	15 - 468	
HBSAQ64	64	530344	1 - 296	15 - 310	
HBSDB50	65	571365	1 - 353	15 - 367	
HBSDB63	66	745211	1 - 331	15 - 345	AP000689, AC006344, and AL096701.
HBSDD91	67	775313	1 - 136	15 - 150	AA069743, and AA069767.
HCDAA94	68	661278	1 - 265	15 - 279	AL020995.
HCDAB17	69	530726	1 - 327	15 - 341	AA679229.
HCDAE77	70	533925	1 - 344	15 - 358	AI908895, and AB027251.
HCDAF27	71	592244	1 - 488	15 - 502	
HCDAF29	72	533812	1 - 265	15 - 279	
HCDAF54	73	530529	1 - 421	15 - 435	
HCDAG92	74	724693	1 - 363	15 - 377	
HCDAG95	75	533871	1 - 412	15 - 426	

HCDAH34	76	533870	1 - 390	15 - 404	
HCDAJ67	77	925362	1 - 305	15 - 319	AL049875.
HCDAK93	78	523648	1 - 186	15 - 200	T05398, and AC003029.
HCDAK96	79	960047	1 - 360	15 - 374	
HCDAM34	80	523607	1 - 265	15 - 279	AC005969.
HCDAO32	81	530006	1 - 316	15 - 330	
HCDAT56	82	533881	1 - 651	15 - 665	AA252681, N51549, AI026801, AI202595, AI000893, AW450220, W44769, AA923523, AI346827, AW090676, AI640582, AI659843, F22685, AI092608, AW102828, AA075433, AI350733, AA789132, N32022, N98535, N69933, and AL109657.
HCDBO13	83	709590	1 - 242	15 - 256	
HCDBR37	84	968501	1 - 329	15 - 343	AB011101, and AF106069.
HCDBR39	85	921893	1 - 347	15 - 361	
HCDBU77	86	661272	1 - 185	15 - 199	
HCDBW51	87	556469	1 - 281	15 - 295	
HCDBW61	88	960044	1 - 203	15 - 217	N51115.
HCDXB78	89	847580	1 - 243	15 - 257	Y18642.
HCDXB84	90	670159	1 - 248	15 - 262	AI244405, AW072090, AA565081, AI253256, H64704, AW026742, AA243715, AW025779, AA455006, AA455005, AW117348, AI767598, AI206307, N46194, AA644147, AI420462, AL035634, AF076957, AF121859, and AF131214.
HCDCE48	91	529893	1 - 334	15 - 348	
HCDCE62	92	523582	1 - 226	15 - 240	AL031177.
HCDCF11	93	967768	1 - 243	15 - 257	AA844561, AA975423, AW173039, AI400317, AA937116, AI863192, AC006942, AC005758, and AL022170.
HCDCK07	94	865908	1 - 149	15 - 163	H89524.
HCDCK91	95	592465	1 - 255	15 - 269	AI268324.
HCDCR26	96	960048	1 - 307	15 - 321	AP000087, and AP000226.
HCDCX68	97	529778	1 - 103	15 - 117	AC003692.
HCDCY13	98	921702	1 - 60	15 - 74	
HCDDBS2	99	847581	1 - 332	15 - 346	AA535216, AA586656, AA565319, AI251584, AI431434, AW192065, AA654781, AI537458, AI537538, AA303040, F13749, AI884383, F23258, AI355986, R33941, AI682665, AA484208, AI708005, AA603530, AA338289, AA639946, AA608751, AI280771, AW079664, AA487690, AA659608, AW068316, AI814739, AI475954, AW162288, AA845209, AC005015, AC006487, AC002126, AC005071, AC005048,

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HCDD62	100	529890	1 - 240	15 - 254	
HCDD161	101	529937	1 - 103	15 - 117	AL248455, and AC005876.
HCDDU07	102	954177	1 - 200	15 - 214	AC005498.
HCDDV90	103	847575	1 - 241	15 - 255	
HCDDY57	104	556465	1 - 349	15 - 363	
HCDDZ09	105	523605	1 - 396	15 - 410	Z83820, AL022574, AP000261, AP000035, AP000100, and Z69722.
HCDDZ44	106	863388	1 - 484	15 - 498	

HCDEB49	107	847572	1 - 238	15 - 252	
HCDEB78	108	921710	1 - 125	15 - 139	
HCDEG67	109	531239	1 - 454	15 - 468	
HCDEG95	110	533879	1 - 467	15 - 481	
HCDEI16	111	667338	1 - 310	15 - 324	AC008064.
HCDEI29	112	523506	1 - 198	15 - 212	
HCDEI89	113	524045	1 - 341	15 - 355	
HFIAB89	114	848927	1 - 57	15 - 71	
HFIAB93	115	713799	1 - 592	15 - 606	AW299250, AW438583, AI261419, AI271941, AA688176, W19548, AI867634, N62642, AI718356, T59367, and AC005179.
HFIAB82	116	779898	1 - 437	15 - 451	
HFIAB10	117	964652	1 - 222	15 - 236	
HFIAB07	118	952884	1 - 528	15 - 542	H75698, and AC005722.
HFIAP31	119	697775	1 - 340	15 - 354	AI394725, T49120, AC004916, AP001052, and AP001051.
HFIAP89	120	587844	1 - 335	15 - 349	
HFIAP91	121	925831	1 - 603	15 - 617	AI754091, AI991838, AW005052, AW054864, AA603953, AA604330, AI147846, AI570396, AI497756, AI421847, AA877182, AI494281, N35004, AA775287, W46449, AA581458, AI086636, AI148897, AI278835, AA057575, AW168484, AW272886, R61553, AW196844, AI888235, AI679184, AW192289, H99897, W52277, AI356673, AA428604, AA969120, AI086886, AW167037, W47555, N69430, AA972050, AA579776, N93836, AI744805, W88660, F30196, H67841, AA703585, R54415, H80849, AA496690, AA777896, AA234453, AA035655, AA350919, F37094, AA234061, AA284876, T93624, AI474971, AA886060, F31971, AA150893, AA300810, AA376247, AW014654, AA977993, AA496609, H67163, AI310732, AI755278, AA430492, AA993506, AA558203, F31374, AA430533, AA477605, AA436330, AA410238, AI086193, H54089, AA682577, AI342640, AI161001, AI089475, AA290638, AA502644, AA402631, AW151250, AI045805, AA676716, U46298, AA724973, F36499, W52276, AA329392, W88866, T74861, AI659749, AA432307, W47495, W40292, AA419293, H38512, AA057574, AA203205, AI110156, AC002094, AF077203, and AC002324.
HFIAB83	122	780358	1 - 190	15 - 204	
HFIAB63	123	966761	1 - 543	15 - 557	AI676091, and AC012039.
HFIAB48	124	587871	1 - 414	15 - 428	
HFIAB06	125	934675	1 - 430	15 - 444	AA452688, H91923, R18017, R69518, R74244, C04901, W73580, AA315530,

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HFICE40	126	587918	1 - 441	15 - 455	
HFICF01	127	916103	1 - 199	15 - 213	
HFICI52	128	522239	1 - 635	15 - 649	AW303375, AW173315, AA417652, AI751258, AA364833, C05155, AA600736, AI090486, AA258414, AA625303, C04206, AA455496, AI768270, AA599207, AA446297, C03119, AA421744, AI828437, AI862133, AA834031, AA024968, AA446024, AA419609, AA419525, AI272646, AI148235, AA634323, AI092202, AA455497, AI191710, AA593295, AI218226, AA319726, AI754332, AI039656, AA774270, AA336003, AA384793, AI350380, AA978105, AI084698, AA912802, N64555, AI751035, AI673545, N67061, AI432010, AI754989, AA971661, D31528, AI609700, AA478719, AI221431, AI075349, AA456579, AW338252, AA375571, AA936765, AA610296, AA258397, T59227, AI564218, D31541, T59268, I76208, and AR020615.
HFICM95	129	587875	1 - 431	15 - 445	
HFICZ77	130	934192	1 - 323	15 - 337	AI803895, AI391495, AA974333, AA480293, AI418615, AW303930, AA976516, AI376344, AA027959, AI188582, AA772607, AA150835, N49399, W43008, AI073381, AI679130, AI679704, AA558944, AA748509, AA854570, AI084408, AA863284, AI094952, AI351871, AI271532, AA994580, AI370805, AI401404, AW044595, AI214656, R33818, AA772710, W95681, AA993489, AI023527, AA025063, AA456325, AI563920, AI887313, AA976183, W07752, AA683499, AA873879, AA894918, AA737975, AI432209, N80691, AI299818, AA991522, AA975924, AA047682, AA906771, AA665526, AI151172, AI379259, R33819, AI707592, AA984396, AA047733, AA025062, W45208, AI095417, AA662634, AI147183, C02347, F34897, AA972351, AI041404, AW024289, AA683598, AW027714, AW366247, AI119399, AW008226, AI277938, AI261589, AI499570, AW079334, AA910330, AI638644, AW166412, AI561177, AI884318, AI364167, AI042544, AI266652, AI419826, AW192461, AI275609, AW081383, AW087934, AI630947, AI037602, AI538564, AI037582, AI445829, AI934011, AI963763, AI679771, N29277, AI744268, AI370623, AA806720, AI421149, AI473536, AI633125, AI568293, AI916419, AW152182, AI345415, AA580663, AW129264, AI620864, AI522052, AI698391, AW148882, AI538850, AI648509, AI363741, AI860348, AI042382, AW089844, AI539690, AI701097, AW190194, AI524626, AA019328, AI374987, AI352514, AI679891, AW198090, AI371243, AI125015,

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HFIDB12	131	968922	1 - 616	15 - 630	
HFIDL94	132	964316	1 - 390	15 - 404	

HFIDM69	133	926894	1 - 473	15 - 487	R31339, and AA251156.
HFIDN81	134	959050	1 - 441	15 - 455	
HFIEC13	135	883185	1 - 511	15 - 525	Z59127.
HFIEF04	136	926824	1 - 98	15 - 112	Z99396, AL036418, AL038837, AL037051, AL036725, AA631969, AW392670, AL039074, AW372827, AL038509, AL036924, U46341, AL036858, AW384394, AL039564, AL119497, AL039085, AW363220, AL039156, AL039108, AL039109, AL039128, AL119341, AL037639, AL119443, AL037094, AL039659, AL119457, AL134524, AL119319, AL119355, AL036196, AL036190, AL119324, AL119496, AL119483, AL119484, AL119363, AL119391, AL042965, AL038531, AL119335, U46350, AL037526, AL036767, AL119522, AL037082, AL119396, U46351, U46349, AL039625, AL039648, AL045337, AL119418, AL036238, AL038447, U46346, AL042978, AL042909, AL119444, AL042433, AL039678, AL039629, AL134902, U46347, AL037085, AL039386, AL036268, AL038520, AL134528, AL134920, AL039423, AL042551, AL037615, AL039150, AL037077, AL037205, AL042614, AL040992, AL119439, AL042984, AL042975, U46345, AL119399, AL119401, AL134536, AL036998, AL036733, AL119412, AL134531, AL119464, AL042450, AL134525, AL134538, AL042544, AL119413, AL043019, AL042970, AL119488, AL037027, AL037178, AL043029, AL039410, AL042973, AL036679, AL036719, AL043003, AL042542, AL042850, AL119413, AL036191, AL036765, AL037021, AL036774, AL036886, AL036158, AL036999, AL036836, AR066494, AR060234, AR069079, A81671, AR023813, AR064707, AR054110, and AB026436.
HFIEH79	137	855196	1 - 628	15 - 642	Z99396, AL038837, AL037051, AL036725, AL039074, AA631969, AL039085, AL039564, AL039156, AL039108, AL039109, AL039128, AL039659, AL038531, AL039625, AL039648, AL045337, AL037526, AL039678, AL039629, AL039150, AL039423, AL036924, AL040992, AL042909, AL037639, AL037094, AL037726, AL038447, AL039410, AL036858, AL036238, AL036190, AL036196, AL119483, AL036767, AL045353, AL037615, AL036973, AL038851, AL037082, AL119484, AL039440, AL044407, AL036418, AL038509, AL036268, AL036117, AL037077, AL039386, AL134524, AL036733, AL036998, AL039924, AL037027, AL036679, AL119418, AW392670, AL036191, AL037178, AL036719, AL037085, AL037021, AL037054, AL039538, AW384394, AL119341, AL038520, AL036765, AL119497, AL044530, AL036999, AW372827, AW363220, AL119363, U46350, AL119319, AL119457, AL036158, AL119443, AL037016, AL119324, AL119444, AL119335, AL119391, AL119355, AL119522, U46349, U46341, AL038821, U46351, AL119496, AL119396, AL036836, U46347, AL036964, AL119439, AL037205,

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HFIB16	138	661971	1 - 458	15 - 472		
HFID91	139	702324	1 - 721	15 - 735		N31707.
HFIF47	140	857988	1 - 1959	15 - 1973		AA534198, AI978627, AW166513, AI459812, AW166498, AI819341, AW195142, AI139595, AA209319, AI365580, AI620649, AI022352, AA583627, AW005402, AA583619, AI475193, AW166054, AI569467, AI540081, AI191668, AA331346, AI272323, R51977, AA508608, AA678590, AA524450, AW451651, AI090886, AW082159, F09189, R51978, AA378790, AI382250, AI378098, AI917676, AI868588, T46979, AI355097, AI635445, AW131365, F11527, AI291485, N64277, and T46978.
HFIF63	141	944246	1 - 750	15 - 764		AW182823, AI378016, AI669104, AI420515, AA010826, W95509, AW297177, W95412, AA011202, AA782437, AI869000, AI702739, AA450119, AA889785, AA255554, and AI291551.
HFII60	142	740280	1 - 456	15 - 470		
HFII85	143	707899	1 - 548	15 - 562		
HFII29	144	690546	1 - 367	15 - 381		
HFIS76	145	769952	1 - 390	15 - 404		
HFIZ33	146	588058	1 - 496	15 - 510		AA054673, H89424, AA180830, and AF025422.
HFIZ51	147	725587	1 - 370	15 - 384		
HFIB73	148	669594	1 - 438	15 - 452		AL031296.
HFIS21	149	670765	1 - 529	15 - 543		AI570906, AL118651, AL118594, AA644545, AL050343, AL133445, AL096791, Z93023, AC004020, AC004851, AC007450, AC000353, AL132712, AP000704, AC002400, AC004491, U91323, AL021579, AL022334, AL020997, AC005899, AL034417, AC002565, AL009181, AC004106, AC007298, AL139054, AC006449, AC002425, AC002544, AL109865, AL022313, AI246003, AC007227, AC005071, AC006014, AC006285, AC005529, AC005488, AF205588, Z95152, AP000689, AL034419, U73640, AC004966, AC004477, AL035450, AL031577, AL133448, AC008372, AC003036, AC004685, AL009183, AC006013, AC005326, AC005225, AL117352, AP000240, AL049829, AC007773, AC004526, AP000047, Z85986, AC008115, AC005520, AC016025, AL121658, AC004638, AD000092, AL049795,

						AC00448, AC005015, Z98304, AC007050, AC003029, AC003101, AC007226, AC006965, and AC012384.
HFJUF34	150	703972	1 - 448	15 - 462		
HFJTX48	151	934328	1 - 453	15 - 467		
HFJTZ24	152	677144	1 - 412	15 - 426		AJ011930, AJ011931, and AP000219.
HFJUE17	153	855119	1 - 452	15 - 466		
HFJUH54	154	929787	1 - 429	15 - 443		AW295133.
HFJUI66	155	746397	1 - 304	15 - 318		AC004774.
HFJUI95	156	735969	1 - 425	15 - 439		
HFJUM59	157	724249	1 - 308	15 - 322		AC009044.
HFJUE63	158	691921	1 - 476	15 - 490		
HFJUP04	159	582296	1 - 158	15 - 172		R64316.
						R64259, AA344341, AJ080039, AL046624, AA629791, AI368952, AW168763, AI952419, N26238, AA834946, AI524512, AI264761, AA393317, AI092959, N34467, AI167603, AI817019, AI186197, AW024266, AA220934, AI686547, AA079792, AI423180, AW294323, AI022487, AA298287, AI125828, AA977969, AI041033, AW167771, AI982550, AA577038, AW129990, AI219200, AI745726, AI872119, AA568591, AI074179, N23849, AI076303, AI126251, AI873831, H89854, AW410097, N73002, AA034187, AI077832, AI144021, AA961792, AA431977, AI818881, AI620483, AI827251, AA738013, AW450235, AI277544, AI049595, AA738259, AI263352, AI193279, R85594, AW351844, N52553, T57796, AI000731, AW177690, AI018741, AI125766, AA744959, AI351749, AI753417, AI865588, N76513, H71780, F25828, AI971511, AW389860, AA805498, AI699779, AW054724, AA417958, AI754465, AI189605, AA846282, H71692, N58371, AW028940, AI168778, AA033792, R85377, AL134572, AA702274, AA001869, AA371623, AI270649, AA704581, AA342144, T79160, AA151314, F00140, T99810, H90753, H42220, AA903483, AA700585, AA932956, AI557195, AI143854, AA682817, T95829, AL110192, AL050150, AF077054, AB020692, AL096773, X60127, and X52311.
HFIVB03	160	924021	1 - 324	15 - 338		
HFIVB25	161	678022	1 - 269	15 - 283		AA004777, T66806, AA033897, R75757, and AB014550.
HFIVB62	162	741665	1 - 241	15 - 255		AC004002.
HFIVQ02	163	919802	1 - 441	15 - 455		
HFIXA30	164	692637	1 - 313	15 - 327		AI038502, AA993051, AI926924, AA836474, and AW269412.
HFIXC30	165	692635	1 - 345	15 - 359		

HFIXC44	166	839536	1 - 541	15 - 555	R52856, R16202, H09464, R16204, D53134, Z42545, T66661, and T66663.
HFIXC49	167	722886	1 - 369	15 - 383	
HFIXK83	168	767156	1 - 351	15 - 365	
HFIXK94	169	943717	1 - 412	15 - 426	
HFIXM11	170	966714	1 - 218	15 - 232	AF045448, and AF064860.
HFIXO03	171	923735	1 - 361	15 - 375	AA824654, AA810370, AA644538, AA824655, AA521376, AA649705, AA834755, C14793, H02877, AA483223, AA574110, AA704643, AA678436, AA640034, AA568778, AA858197, AA503473, AA973803, AA515909, AA719080, AA446657, AA906889, AA679009, AA577906, AA602528, AA605032, AA582911, AA804379, AA601355, T49241, AA721981, AA235466, AA668578, AA348504, AA533036, AA483731, T53128, AA910125, AA425922, AA573020, AA522942, AA533725, AA490183, AA304977, AA341336, AA527958, AA143490, AA838096, AA525249, AA668902, AA558616, AA191198, AA156538, AA578017, AA663486, AA434388, AA670468, AA525876, AA601499, AA846929, AA102006, AA053551, AA633094, AA403110, T16056, W16581, AA600222, AA623002, AA861959, AA280632, AA437161, AA831904, AA845843, AA127636, AA825357, AA873560, AA665021, AA630925, W05364, AA682912, AA521355, AA678453, AA564859, AA487225, AA401022, AA461206, AA599920, AA708311, AA649722, AA127517, AA524838, AA210852, AA847984, AA972238, AA654761, AA487858, AA644207, AA970213, T10560, R32415, AA169756, A1191227, AA634145, AA635442, AA524809, AA551201, AA325699, AA714595, AA595825, F32800, AA486885, AA808941, N46153, AA357307, AA059472, AA523815, AA664015, F09736, N69316, AA167643, AA134347, AA780515, AA569743, AA650271, AA715355, AA720691, H48636, AA678772, AA515435, AA629827, AA987619, AA729740, AA309196, T94075, AA768905, F23250, AA480790, AA767376, M85966, AA828042, AA728889, AA346575, AA604497, AA633266, AA095511, AA630606, AW088058, M77899, AA492140, A1002834, AA778110, AA613851, R95704, AA631799, T15897, AA081909, AA825455, T24049, AA405453, H02135, AA326589, AA434484, H11124, AA744338, AA834756, AA632755, AA774184, AA113376, AA486414, AL046457, AA788726, X62695, AP000302, AP000114, AP000046, Z83313, Z68192, AP000431, L43392, AF029750, AB012251, Z92844, AC004047, AC004216, AL031012, U07000, AC005755, S61977, AC006515, U67274, U20770, Y12508, M87919, AC004837, AL109798, AP000548, AL022325, AL031588, AC006466, AF193806, AC003681, U02044, U55180, A26236, L04965, AP000501, AL132712, L44140, AC007878, U14694, U13056, D49685, AL096765, AF112866,

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HFIXV93	172	597031	1 - 361	15 - 375	AL080075.
HFIXY13	173	656812	1 - 347	15 - 361	R54797.
HFIXY57	174	734580	1 - 352	15 - 366	
HFIXY80	175	965077	1 - 395	15 - 409	AA833709, AL342422, AL207067, AW303434, AW005730, and AW002395.
HFITYA86	176	757155	1 - 343	15 - 357	AF015720, AF015722, and AJ229041.
HFITYB24	177	952847	1 - 291	15 - 305	AL022724.
HFITYB40	178	964251	1 - 428	15 - 442	
HFITYK01	179	916125	1 - 154	15 - 168	W22304, and AC007510.

HFIYL01	180	919416	1 - 418	15 - 432	R69518, AA452688, AA315530, R74244, H91923, C04901, AA159260, R18017, W73580, H28250, W84825, R49760, R83609, AA486811, N53738, H84664, T64564, T79349, H24652, AA931976, C05147, H92397, R62673, and H25249.
HFIYO14	181	657598	1 - 281	15 - 295	AA927326.
HFIYP02	182	919501	1 - 363	15 - 377	
HFIYV01	183	916064	1 - 413	15 - 427	AI799462.
HFIYV03	184	923755	1 - 389	15 - 403	Z97206, and AL034375.
HFIYV59	185	861487	1 - 317	15 - 331	AA502207, AW188742, AA668896, AI355246, AL037771, AA975997, AA668915, AW023111, F35684, R64617, AA535736, AA536040, AI653999, AI791131, AA494174, AI791130, AA857518, AL119563, T05118, AA487209, AA364860, AA906536, F34170, AA084609, H47295, AL040009, AI446336, AI434513, AA676971, AA578690, AA581525, AA486565, AA309341, T71936, AI189682, AA483606, AA225273, AA737235, AA846923, AA991914, AA485328, AA630535, R89560, AA904211, AA689351, H07953, AL041375, AA630122, AI206841, AA983673, AA502532, AI866911, AA312303, AA654801, AW316777, AW020736, AA709362, N24909, AW192402, N55296, AL031730, AF205588, AC007637, AL031005, AC004477, AL109963, AC004000, AC004491, AL021937, AC004841, AC005740, AL049758, AL049636, AL117337, AC005670, U91326, AC005899, AL096791, AC007227, U96629, AL139054, AC004859, Z98946, AC002070, U91323, AC005696, AC005412, AF047825, U73024, Z95331, U80017, AC002301, AL031666, AC005317, AC002425, AF000689, AC005911, AC005089, AC005971, AC003098, AL022163, U78027, AC004525, AC005225, AC004921, AC008044, AC004922, AF001552, Z84480, AL135744, AC002094, AC004967, AF111168, AC003962, AJ246003, AC006512, AC005480, AL136295, AL035422, AL049843, AC005839, AL096701, AC006211, AC005183, AC005316, L78810, AL035249, AP000344, AP000555, AC005914, AC007376, AC005532, AC005523, AL021578, AC002477, AC004912, AC007546, AC005988, AL035587, AL049539, AC005704, AL078581, AL035417, AB003151, AC006101, U07561, AC005730, AP000557, Z84487, AL109758, AC008372, AL008726, AC004876, AC004134, AC005722, AC007686, AC002126, Z98750, AJ010770, AC005531, AC006441, AC004985, AC004895, AC004263, AC004383, AL031295, AL121658, AC005632, AC006120, AC008040, AC005043, AL109984, AC002430, Z99716, AC004966, AL035090, AF196779, AC005921, AL080243, AP000208, AC006505, AF117829, Z84466, AC006011, AB023051, AL049757, AC005261, AL009181, AC005562, AL035086, AL132777, AC002133, AL022318, AC007193, AP000066, AC005902, AC007384,

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HFYW08	186	958978	1 - 472	15 - 486	
HFYZ13	187	656795	1 - 364	15 - 378	
HFIZF95	188	795734	1 - 351	15 - 365	AI470647, and R26573.
HFIZG93	189	928170	1 - 537	15 - 551	AW070612.
HFIZH29	190	953895	1 - 390	15 - 404	
HFIZM92	191	791267	1 - 559	15 - 573	HI13123, R82393, AI634609, AI925440, AI333038, AW195580, AA504939, AB014580, and AL049844.
HFOXA79	192	774901	1 - 238	15 - 252	AC004150.
HFOXB85	193	752957	1 - 362	15 - 376	AL133500.
HFOXC25	194	677995	1 - 335	15 - 349	AC012039.
HFOXC35	195	638311	1 - 560	15 - 574	AI284640, AA847499, AI499588, AI754336, AI802835, AA601876, AL138396, F12561, AA728812, AI862939, AA847952, AA368059, AA358515, AA765736, AA514854, AI002510, F25733, AI537077, AA126450, AA508359, AI282511, AA620467, F08248, AW327868, AA935988, AL121235, C06339, N35602, AW028392, AA045017, AI338350, AA629992, AI079389, AA780784, AA724333, AA169263, AI093030, AI933534, AA493708, AA659360, AI536900, AA579075, AA719292, AL045808, AL046156, AI358812, AA347027, AA847515, AI312309, H71429, AA683258, AA491862, AA491831, AI564185, AW168618, AI921061, AA491650, AW075948, AL042853, AI290405, AW023149, AA368943, AI061143, AI076766, AA071393, AA679936, AA634196, AI610435, AI866964, AA351056,

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HFOX83	196	587955	1 - 271	15 - 285	AA928539, AI590043, AI863382, AI345415, AA830709, AI690813, AI679388, AA641818, AI612913, AI819545, AI491842, AW162194, AI954200, AW169291, AL047100, AI345612, AI452560, AI479292, AI345416, AI613038, AW198090, AI571439, AI702063, AA937566, AI859991, AI370623, AI635851, AI554402, AI376425, AW129722, AI885664, AL048538, AW084896, AI538850, AI540831, AI698391, R40363, AA804541, AI635216, AL120706, AL043166, AI863002, AI633125, AW130362, AI696714, AI909697, AI539800, AI927233, AI599260,

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HFOXLO3	197	923772	1 - 309	15 - 323	AI394067, and AI056068.
HFOXMS4	198	587974	1 - 346	15 - 360	
HFOXN89	199	587984	1 - 97	15 - 111	
HFOXO24	200	733377	1 - 517	15 - 531	AI026814.
HFOXR28	201	587994	1 - 310	15 - 324	
HFOXRP67	202	806488	1 - 447	15 - 461	D56451, AI797289, AW008969, AI394269, AI541453, D56220, Z36872, H17761, AW009897, AA248589, AI278793, H59335, C04806, R01796, AW062936, N30347, H93411, AW263105, R62171, AW178925, AA613553, AI148761, AA960959, R52799, AA996071, AW363731, AI026967, AW069303, AA148228, AW247577, H41429, N91665, AA837473, AW247732, R86909, T34155, C05230, AA316485, N94214, AI751446, AI750270, AI276480, AA865609, T36130, R81681, N93270, AI383153, AF153605, and AF151861.
HFOXSR1	203	588052	1 - 502	15 - 516	AC009509.
HFOXU83	204	887781	1 - 334	15 - 348	
HFOXU92	205	588057	1 - 64	15 - 78	AA225747.
HFOXV15	206	964296	1 - 451	15 - 465	AR038762.
HFOXV80	207	771290	1 - 442	15 - 456	AA308546, AW157090, AI937913, AW156893, AW162217, AW157724, AW161439, AI879643, AW156973, AI879261, AW163058, AI929716, AW087100, AA305024, AW157680, AW068829, AI929159, AW160392, AI928949, AI929458, AI879102, AI815607, AW163676, AI816107, AI929203, AA533150, AA603376, AA315102, AA557858, AI042255, AA316902, AA305999, AI929416, AA467847, F20887, AI148106, AA635409, AI080578, C16701, AI735002, AI703215, AI218297, AA578143, AA306384, C15041, AI004923, F34246, AI813679, AW161950, AI741580, AA558231, F27426, AA315107, AA316386, F28430, AA747217, F19264, AA582173, AW162077, AI880659, AI284407, AA969828, AA316519, AI797882, AA182966, AA312837, AA593697, AA429825, AA314832, AA534268, AW051532, AA551986, AA514368, AI283754, AA314733, AA857416, AA504055, AA099703, AA703668, AA813296, AA305425, AA627106, AA658158, AA102518, AA912491,

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HFOYI36	208	935532	1 - 412	15 - 426	
HFOYL77	209	494844	1 - 303	15 - 317	
HMUBM2	210	908912	1 - 551	15 - 565	
6					
HMUBX25	211	678004	1 - 248	15 - 262	
HMUBY88	212	740311	1 - 360	15 - 374	D31124.
HOAAB15	213	575254	1 - 283	15 - 297	
HOAAB42	214	530605	1 - 246	15 - 260	AL047846, AC008013, AC009533, and AR050956.
HOAAB56	215	507839	1 - 361	15 - 375	
HOAAC31	216	693597	1 - 368	15 - 382	AA648984, AA866183, and AA236595.
HOAAD05	217	932756	1 - 546	15 - 560	AL045968, AL046394, AW449989, AI351357, AA757688, AI937374, AI129540,

HOAAD52	218	859628	1 - 317	15 - 331	AI952327, W28986, AI362659, AA704558, AA973323, AP000219, and AJ239328.
HOAAE10	219	968532	1 - 325	15 - 339	AC005164.
HOAAE45	220	530602	1 - 316	15 - 330	
HOAAE49	221	859630	1 - 290	15 - 304	AI696455, AA631512, AA280198, AA063419, AA730609, AA063493, N53783, AJ230815, AA094679, AI919048, T03774, AI547110, AA676462, AA484321, T94858, AI800189, AI683125, N64807, N63562, AI832554, AA338436, AA325104, AA485778, AW169324, H63173, AA229489, AA297208, AW085626, AA284638, AA720594, AA640104, C15279, AW192471, AI754926, T58562, AA594164, AA524804, AA524604, AA115769, AA302962, AI267285, AA362670, AA228268, R43468, AW086015, AA730325, AI523991, AW085751, H65404, AI708663, AA452912, AA516061, AA910236, AI299889, AA494145, AW169183, AA632355, AA507657, AI818921, AL079682, AL041740, AA358330, AA174108, AW089646, AA300221, H60396, AA082007, AI242994, AI207692, W02485, W45215, AL109984, AL035423, AC005763, AC006343, AC007225, AC006930, AC005231, AL020995, AB001523, AL021393, AC011594, AC005179, Z69364, AL034379, AC002316, AL135745, AC005775, AC001231, AC005082, AC007066, AC004106, AC019014, AC005694, AC003969, X64467, AB026906, AC005593, AC006205, AC004844, AC007238, AD000092, Y18000, AC005225, AC007686, AC005971, AC005527, AC003658, AC005695, AC004525, AC002463, AC006064, AC005277, Z93241, AL133243, AC005529, AC004033, AC007298, AC004686, AC005215, AL021391, AP000228, AC005412, AL031844, AC002070, AF169035, AP000140, AL022316, AF135028, Z85988, AC004447, AC004650, AL035420, AC004022, AL034417, AC008044, Z82188, AL031432, AL078474, AF064861, AC002504, AC004843, AL096678, AC006011, AC004765, AC010722, AC003013, AL117340, AL109628, AC004388, AF036121, AF196972, Z68756, AC005738, AC006120, AC003685, AC005516, AP000310, AL096703, AL035249, AP000116, AP000152, AP000010, Z97632, AC008085, AP000088, AC003041, AL080276, AC002350, AC005369, AL049709, AL022311, AC007050, AF184614, AC005331, AC005102, AC005410, AC005832, AC007240, AC006148, AC004816, AC007546, AC002076, AC006441, AC005937, AC004073, AB023048, AC005962, Z83844, AF069491, L78833, AC007971, Z83843, Z98946, AL033392, AL078581, AF196969, AL049631, U85195, AC000134, AP000335, AC004019, AL021453, AC002351, AL035658, AC007868, AL031680, AL022165, AC005768, AC006130, AL080242, AF081795, AE000658, AL024498, AL021808, U80459, AC003004, AB022785, AC005933,

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HOAAE73	222	960631	1 - 303	15 - 317		
HOAAF18	223	530600	1 - 343	15 - 357		
HOAAH10	224	968368	1 - 608	15 - 622		AI038589, H38572, AA604708, and H59854.
HOAAI05	225	932537	1 - 296	15 - 310		
HOAAJ23	226	531389	1 - 257	15 - 271		
HOAAK90	227	527490	1 - 280	15 - 294		
HOAAM0 8	228	960060	1 - 189	15 - 203		
HOAAR14	229	526530	1 - 230	15 - 244		H60486, H60440, AW151194, AW378516, AW378511, AC005696, AL031230, AC004771, AC006011, AL049872, AL096701, AC005034, AC003103, AC004983, AC004000, AP000696, AL109952, AL110122, Z99716, AC005031, AC005839, AF196970, AL023575, AL035458, AC004999, L78833, AC006441, AC004859, AL034548, AL023553, AC007390, U80017, AC005399, AC008372, M17262, AL035398, Z85986, AP000512, AL031680, AC004832, AC004797, and AC007182.
HOAAV23	230	527489	1 - 294	15 - 308		
HOAAW2 1	231	527487	1 - 296	15 - 310		
HOAAZ61	232	531065	1 - 320	15 - 334		
HOABA20	233	932539	1 - 104	15 - 118		
HOABA93	234	792929	1 - 198	15 - 212		
HOABD58	235	738359	1 - 96	15 - 110		
HOABP66	236	507175	1 - 277	15 - 291		
HOABP69	237	531049	1 - 98	15 - 112		
HOABR40	238	531051	1 - 344	15 - 358		
HOEAK21	239	954961	1 - 326	15 - 340		
HOEAY14	240	659258	1 - 336	15 - 350		AA010406, and AA513951.
HOEBL44	241	715851	1 - 288	15 - 302		
HOEBQ31	242	693689	1 - 335	15 - 349		
HOEBP01	243	916957	1 - 565	15 - 579		R51124, R50890, H09201, F08412, H10008, R23547, and AC007688.

HOECN79	244	723113	1 - 223	15 - 237	
HOECY54	245	506692	1 - 532	15 - 546	
HOEDD40	246	572900	1 - 332	15 - 346	
HOEDD83	247	578934	1 - 311	15 - 325	
HOEDK10	248	915054	1 - 314	15 - 328	
HOEDT31	249	826009	1 - 461	15 - 475	N40134, AA459424, H23811, AA477809, AW361971, R22603, R80171, AA255699, AW388174, R07949, H43071, AA019983, AA491397, AA853328, AW167516, AA325547, AA156738, AW388175, N42726, AA333808, AA953943, AA299231, N41696, AA715394, T73669, AW083486, T63684, AA838699, AI890778, AA046378, AW008861, AW162991, AW300924, AI205997, H38711, AI125503, AW166548, AA911687, AA504780, AA434314, AI567841, R78822, and R67144. AI954403.
HOEDU54	250	506576	1 - 501	15 - 515	
HOEDU68	251	713695	1 - 156	15 - 170	
HOEEB63	252	745039	1 - 299	15 - 313	R47912.
HOEEC02	253	919822	1 - 226	15 - 240	
HOEOA45	254	717754	1 - 336	15 - 350	Z64883.
HOEEQ17	255	663719	1 - 357	15 - 371	
HOEFG22	256	744340	1 - 272	15 - 286	
HOEFL91	257	790134	1 - 346	15 - 360	AI042148, T72500, D45636, and AL049830.
HOEFN92	258	698444	1 - 312	15 - 326	R45895, AA585325, T18597, R28965, R29218, R28892, D54897, D60765, D60844, AA170832, AA585098, R28735, R29445, R29657, R28967, Z32887, D57491, D59751, AA585101, Z32822, AA585439, AA283326, C15406, D53161, AI547250, D61185, C15069, Z33559, AI546831, AA585476, D61254, AI525316, AI557262, C16294, C16315, D55233, AI557864, R28895, Z28355, D59458, AI541356, AI525306, AI546875, AI557734, AI525500, D59436, AI546999, AI546921, D54850, AI526078, AI526016, AA585155, AI526140, AI541365, AI557740, C16296, C16292, D53447, AI546971, C15120, C15762, AI557763, D52835, C16305, C16293, AI547122, AI557799, AI541383, D53472, AI546901, AI526194, AI526184, AI526109, AI535639, AI557718, AI541517, AI547039, C15737, R29179, AI541374, C16300, AI525339, AI557731, AI526112, AI541205, AI526117, AI526191, AI525556, D57186, AI557787, AI535660, AI546945, AI557727, AI547202, AI541535, AI525431, AI557808, AA585430, AI557809, AI557852, AI547006, D60730, AI541346, AI541013, AA585356, AI540903, AI541307, AI557084, AI540967, AI541034, AI557264, AI557758, AI557807, AI525320, Z30131,

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HOEFS83	259	615154	1 - 240	15 - 254	AL133353.
HOEJE18	260	666349	1 - 300	15 - 314	
HOEJG04	261	859251	1 - 470	15 - 484	AA1997.
HOEJW84	262	859225	1 - 511	15 - 525	R06873, and T84693.
HOEKH88	263	924112	1 - 692	15 - 706	AI694533.
HOEKP01	264	918873	1 - 436	15 - 450	AA043660, AA336439, D79158, T32005, Z24843, and AA482531.
HOEKP79	265	963337	1 - 455	15 - 469	AA506744, AA564925, AW080772, AA972523, W24312, N69686, AA501450, AA831345, AA515733, AW029515, AI264579, AI446127, F25580, AA524846, AI300054, W61253, R51582, AI421723, T64444, AL119156, AL119182, AL133353, AC006480, AC006160, AF011889, AC010206, AC008928, AL133163, AC004849, AC004596, AL121653, AL118510, AC008119, AL024498, AL133500, AL109753, AL096701, Z84488, AC004605, AC007684, AB020867, AL021940, AL031295, AL031602, AC003037, AL021368, AC007221, AL031659, Z98048, AL021877, AC005393, U50871, U96409, AF111168, Z95152, and AC003689.
HOEME76	266	974069	1 - 530	15 - 544	AA280295, H19334, AI371007, AA127347, N24841, F09340, AA6355400, N52087, and U60062.
HOEMK02	267	918364	1 - 94	15 - 108	
HOEMQ65	268	922789	1 - 309	15 - 323	
HOEOE25	269	907806	1 - 611	15 - 625	AW182459, AI376825, AI654638, AA866171, AA984176, AA806823, AA743557, AW340266, AA470942, AA470974, AI868578, AA743581, and AA761032.
HOHAA14	270	468867	1 - 371	15 - 385	

HOHAB04	271	665381	1 - 271	15 - 285	AA465435.
HOHAB21	272	670814	1 - 229	15 - 243	
HOHAE68	273	781448	1 - 321	15 - 335	AI751085, AA033678, D30912, and W55850.
HOHAM3 6	274	782043	1 - 539	15 - 553	AA059163, AA864897, H99945, and N64132.
HOHBE48	275	588317	1 - 386	15 - 400	
HOHBF30	276	859046	1 - 504	15 - 518	Z84484, and AC006571.
HOHBL11	277	966720	1 - 464	15 - 478	
HOHBL32	278	588329	1 - 538	15 - 552	
HOHBO79	279	588271	1 - 428	15 - 442	AI638299, AA918485, and AF077660.
HOHBW8 6	280	784723	1 - 264	15 - 278	AC009247.
HOHBX75	281	669536	1 - 493	15 - 507	AI735183.
HOHBY75	282	840109	1 - 413	15 - 427	AI215403, AW297341, Z21179, and AL137348.
HOHCH04	283	859047	1 - 621	15 - 635	
HOHCI05	284	935123	1 - 380	15 - 394	
HOHCM38	285	709295	1 - 416	15 - 430	AA058800, AI268296, N47161, AA303034, and H45390.
HOHCM90	286	703734	1 - 140	15 - 154	
HOHCO85	287	751299	1 - 565	15 - 579	Z21583, and AL096771.
HOHCP35	288	656516	1 - 281	15 - 295	
HOHCQ76	289	825236	1 - 549	15 - 563	
HOHCQ77	290	661480	1 - 103	15 - 117	AP000274, and AP000104.
HOHCV83	291	735685	1 - 289	15 - 303	AI636734, T60940, H01852, AI078143, AI683019, AA854460, R35259, AA541794, N74027, AW167909, AI439676, W63553, AI472070, AI538106, AI332676, AI446259, W67486, AW245354, AA856817, AW152661, AI459617, AA845825, W67485, T49133, AI961232, AL041342, AI149238, AA807579, AA362037, AA565232, AA502813, AI434365, M78026, AA988600, AI127133, AA502498, T07225, H79586, AA471086, R83068, AA559205, AI223968, N68851, R48980, AI679496, N92064, AA702717, AW439625, AI962973, AW439820, N34258, AI859849, AI762302, AA636102, AA551548, N22153, AA572982, AW073498, AI929410, AI753672, AI750950, AC007371, AF165138, Z94277, AC004084, AC004838, AC005520, AC004985, AL008735, AC005751, AC005971, AF029062, AB000876, AC004181, AP000506, AL022313, AB000882, AC004655, AL031178, AC005377, AL022345, AL031584, AF227509, AF108083, AC005660, AC004941,

					AL035415, AC005486, Z98304, AC000049, AL096774, AC004079, AL033504, AC004020, AC007156, AC008372, AF008915, AC004750, AC005568, AC003959, AL050350, AL035410, AC005913, AC004805, AC005412, AC004854, AC002407, AL050318, AL096716, AC007686, AL022311, AL035587, AL096791, AC006368, AL109865, AC003664, AC008040, AF132033, U73630, Z81314, AC006347, AC006130, AL049748, AL096861, AL022400, AC003973, AC005081, AC005837, AC003991, Z72006, AC004797, AL021707, AP000045, AP000113, AL035417, AL079342, AC005043, AC008115, AC004953, AL022302, AL035249, AC005186, AL133163, AC004531, AL109628, AC005262, AC004771, AL021920, AC004967, AC011604, Z99716, AL049779, AC005005, AF043251, Z49236, AC004235, AC004034, AC002450, AF050154, AC005789, AC005233, AC004131, AC004913, AC004070, Z95116, AL049631, AL096712, AL031657, AC007114, AL031281, AF121782, AL022336, AC009275, AC007011, AC004098, Z98949, AC005058, AC006040, AF064857, L47234, AF179633, AL035683, AC012099, AF003529, AC009263, AC004893, AC002544, AP000555, AC004585, AL133245, Z97053, AC002302, AC005274, Z82173, AC005265, AB015355, AL031602, AL049540, AC005067, AC005255, Z98048, AP000502, AL117354, AL008583, AC005754, AL031280, U82671, AC005914, AF047825, AC005534, and AL031053.
HOHCW0	292	919142	1 - 290	15 - 304	
HOHDB11	293	966413	1 - 650	15 - 664	N29990, N36333, AI085776, H25536, H26237, H81879, H96029, N26443, N31186, W03046, W44451, AA037341, AA079718, AA203198, AA424475, AA745282, D82780, C00261, AA249588, and T48492.
HOHDB32	294	698781	1 - 303	15 - 317	
HOHDD23	295	675616	1 - 400	15 - 414	
HOHDF40	296	710748	1 - 357	15 - 371	AA640725, AI333044, AL042761, and AB011158.
HOHDF53	297	727620	1 - 410	15 - 424	
HOHDI48	298	966379	1 - 241	15 - 255	
HOHDY85	299	764155	1 - 407	15 - 421	
HOHDZ61	300	741382	1 - 272	15 - 286	
HOHEA19	301	668208	1 - 385	15 - 399	
HOHEC41	302	712037	1 - 523	15 - 537	AI971892, AI683311, AB033063, and AR065869.
HOHEN50	303	662365	1 - 150	15 - 164	
HOSAB04	304	531565	1 - 310	15 - 324	W61042, AA304276, AA099793, AW369803, AA451642, AI908298, AW369815,

AW369818, AA451620, AW369839, AA192643, AW151982, AI982623, AI857726, AW369763, AI204558, AA320140, W27176, AA319885, AW023791, W27949, AI670119, AI554355, AW051557, AI804785, AW236073, AI799768, AA192644, AA908706, AA888425, AA876810, AA167392, AA577519, AA876691, AA525477, AA879274, AI345444, CI7613, AI075107, AI114490, F34539, AI492852, AA593784, AA738303, F37334, AA566072, N86742, AA886806, AA503355, AA523167, AA541429, AA876872, AI933389, AA877045, AI352526, AW050724, AI536939, AA86558, AA469371, AI694189, AA937272, AI420436, AA542813, W21397, AI418514, AA166702, AA102263, AA522721, AA166638, AA526669, AW273151, AW327392, AA999779, F17050, AI042584, AA136123, AA747343, AF117616, AL031003, L39354, L39338, L39332, U95676, U95677, U95681, L39330, L39334, U95680, U95688, AI230596, AI230597, AI230599, AI230603, AI230605, AI230609, AI230595, AI230602, AI230607, AI230610, AI230611, AI230613, AI230600, M76331, M76289, M76288, M76293, M76360, M76286, M76297, M76320, M76329, M76314, M76363, M76367, M76364, M76366, M76287, M76307, M76342, M76368, M76302, M76339, M76306, U25391, U25395, U25359, U25363, U25371, M76315, M76290, M76323, U25357, U25368, U25400, M76316, U25379, M76341, M76340, U25409, M76301, M76337, M76356, U25358, U25373, U25396, U25407, AF176190, M76296, M76304, M76347, M76348, U25372, U25412, AF176182, M76361, U25390, AF176138, AF176179, AF176180, M76335, M76351, M76354, U25397, M76362, U25369, AF176174, M76305, AF176202, M76328, M76350, U25403, U25408, AF176183, AF176205, M76352, U25364, U25366, AF176161, M76330, U25410, AF176171, AF176172, AF176200, AF176201, M76333, U25388, U25399, U25405, U25406, AF176166, M76292, M76295, M76326, M76359, U25356, U25361, U25384, U25402, U25365, U25370, U25374, U25413, AF176132, AF176181, AF176194, AF176203, M76353, U25362, U25367, U25392, U25393, U25394, U25401, AF176125, AF176140, AF176141, AF176164, AF176178, AF176189, AF176199, U25377, U25378, U25398, AF176130, AF176137, AF176142, AF176158, U25404, AF176139, AF176162, AF176167, AF176175, AF176204, U25354, U25355, AF176131, AF176134, AF176144, AF176159, AF176187, M76309, U25383, AF176126, AF176128, AF176160, AF176163, AF176170, AF176185, AF176198, M76319, AF176129, AF176186, AF176193, M76324, U25381, U25382, AF176143, AF176173, AF176184, AF176133, M76355, M76346, M76299, M76291, M76294, M76312, M76283, X93341, M76325, M76334, V00661, M76303, U25411, AF176156, U25360,				
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